

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:22:25 ; Search time 133.103 Seconds  
(without alignments)  
579.640 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579

Sequence: 1 MNKLYIGNLSENAAPSDLES.....VKHQOQKALGSPQSRRK 579

Scoring table:

OLIGO  
Gapop 60.0, Gapept 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

A\_Geneseq\_101002:\*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	100.0	579	21	AA11328
2	579	100.0	579	23	AB174960
3	377	65.1	579	21	AA11365
4	377	65.1	579	23	AB174997
5	377	65.1	579	23	AB175053
6	377	65.1	579	23	AB175054
7	376	64.9	586	23	AB175048
8	148	23.7	619	22	AB175062
9	89	17.1	148	22	AB175062
10	93	16.1	93	22	AA178238

11	93	16.1	93	22	AA138501	Peptide #12538 enc
12	65	11.2	583	22	AB12592	Novel human diago
13	45	7.8	45	22	AB143427	Peptide #10933 enc
14	45	7.8	45	22	AA164356	Human brain expres
15	45	7.8	45	22	AA137315	Peptide #11352 enc
16	37	6.4	209	22	AB121961	Novel human diago
17	37	6.4	266	22	AB12593	Novel human diago
18	36	6.2	577	22	AA130649	A murine c-myc cod
19	26	4.5	39	22	AB121960	Novel human diago
20	24	4.1	261	22	AA116161	Human novel secret
21	24	4.1	319	22	AA139826	Human polypeptide,
22	20	3.5	20	23	AB175024	Human lung tumour
23	20	3.5	20	23	AB175025	Human lung tumour
24	20	3.5	20	23	AB175026	Human lung tumour
25	20	3.5	20	23	AB175027	Human lung tumour
26	20	3.5	20	23	AB175028	Human lung tumour
27	20	3.5	20	23	AB175029	Human lung tumour
28	20	3.5	20	23	AB175030	Human lung tumour
29	20	3.5	20	23	AB175031	Human lung tumour
30	20	3.5	20	23	AB175032	Human lung tumour
31	20	3.5	20	23	AB175033	Human lung tumour
32	20	3.5	20	23	AB175036	Human lung tumour
33	20	3.5	20	23	AB175037	Human lung tumour
34	20	3.5	20	23	AB175038	Human lung tumour
35	20	3.5	20	23	AB175039	Human lung tumour
36	20	3.5	20	23	AB175040	Human lung tumour
37	20	3.5	20	23	AB175041	Human lung tumour
38	20	3.5	20	23	AB175042	Human lung tumour
39	20	3.5	20	23	AB175043	Human lung tumour
40	20	3.5	20	23	AB175044	Human lung tumour
41	20	3.5	20	23	AB175045	Human lung tumour
42	20	3.5	20	23	AB175046	Human lung tumour
43	20	3.5	20	23	AB175058	Human lung tumour
44	20	3.5	20	23	AB175060	Human lung tumour
45	20	3.5	20	23	AB175061	Human lung tumour

#### ALIGNMENTS

RESULT 1	
AA11328	standard; Protein; 579 AA.
XX	
AC	AA11328;
XX	
DT	21-FEB-2001 (first entry)
XX	
DE	Human lung cancer-associated protein L523S.
XX	
KW	Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW	vaccline; detection.
XX	
OS	Homo sapiens.
XX	
PN	WO200061612-A2.
XX	
FD	19-OCT-2000.
XX	
XX	
PF	03-APR-2000; 2000MO-US08896.
XX	
PR	02-APR-1999; 99US-0285479.
PR	17-DEC-1999; 99US-0466396.
PR	30-DEC-1999; 99US-0476496.
PR	10-JAN-2000; 2000US-0480884.
PR	22-FEB-2000; 2000US-0510376.
XX	
PA	(CORI-) CORIXA CORP.
XX	
FI	Wang T, Fan L;
XX	
DR	WPI; 2000-628399/60.
DR	N-PSDB; AAC65900.



```

Db 301 KIEDDTDKITITISPLQELTLNPERTITVKGAVETCAKAEEIMKKIRESEYENDIASMNL 360
Qy 361 QAHLIPGLNINLALGLPPTSGMPPTSGPPSAMTPPYQFQSESETEYHOFIPALSYGAI 420
Db 361 QAHLIPGLNINLALGLPPTSGMPPTSGPPSAMTPPYQFQSESETEYHOFIPALSYGAI 420
Qy 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMNVTITGPPEAOFKAGRTYIGKIKENFV 480
Db 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMNVTITGPPEAOFKAGRTYIGKIKENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPDENDDVVYKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPDENDDVVYKIT 540
Qy 541 GHFYACQVAORAKIOELITGVKHOQKALOSGPPSRRK 579
Db 541 GHFYACQVAORAKIOELITGVKHOQKALOSGPPSRRK 579

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## RESULT 3

```

ID AAB11365 standard; Protein; 579 AA.
AC AAB11365;
DT 21-FEB-2001 (first entry)
XX Human lung cancer associated antigen L523S.
DE Human lung cancer associated antigen L523S.
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
RV vaccine; detection.
XX Homo sapiens.
OS Homo sapiens.
PM W0200061612-A2.
PD 19-OCT-2000.
XX 03-APR-2000; 2000MO-US08896.
PF 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
PA Wang T, Fan L;
PI WPI: 2000-628399/60.
DR N-PSDB; AAC66035.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PI in a patient -
XX Claim 3; Page 259-261; 261pp: English.
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX Sequence 579 AA;
SO

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Query Match 65.1%; Score 377; DB 21; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MNKLYIGNLSENNAPSDLESIFPKDAKIPVSGFVTKTYGAVFQDPDDESMALKATEALSQ 60
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Qy 61 TELHGKPIEVEHSVPKRQRIKQIINIPPHLOMEVDSLYQGVVESCQVNTDSETA 120
Db 61 TELHGKPIEVEHSVPKRQRIKQIINIPPHLOMEVDSLYQGVVESCQVNTDSETA 120
Qy 121 VVNTYSSKQAOARQALDKLNGFOLNEFTLKVAYIPDEMAAQQNPLOQPRGRGIGQRGSS 180
Db 121 VVNTYSSKQAOARQALDKLNGFOLNEFTLKVAYIPDETAQQNPLOQPRGRGIGQRGSS 180
Qy 181 RQSPGVSQKQPCDLPRLVPTQFVGAIIKGEATIRNITKQTSKIDVHRKENGAA 240
Db 181 RQSPGVSQKQPCDLPRLVPTQFVGAIIKGEATIRNITKQTSKIDVHRKENGAA 240
Qy 241 EKSTITITSTPEGTSACKSSTLEIMKEADIFTEBIEPLKILAHNFPYGRILGKEGRNLK 300
Db 241 EKSTITITSTPEGTSACKSSTLEIMKEADIFTEBIEPLKILAHNFPYGRILGKEGRNLK 300
Qy 301 KIEDDTDKITITISPLQELTLNPERTITVKGAVETCAKAEEIMKKIRESEYENDIASMNL 360
Db 301 KIEDDTDKITITISPLQELTLNPERTITVKGAVETCAKAEEIMKKIRESEYENDIASMNL 360
Qy 361 QAHLIPGLNINLALGLPPTSGMPPTSGPPSAMTPPYQFQSESETEYHOFIPALSYGAI 420
Db 361 QAHLIPGLNINLALGLPPTSGMPPTSGPPSAMTPPYQFQSESETEYHOFIPALSYGAI 420
Qy 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMNVTITGPPEAOFKAGRTYIGKIKENFV 480
Db 421 IKGOGHILKOLSRPAGASTIKIAPAEAPDAKVMNVTITGPPEAOFKAGRTYIGKIKENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPDENDDVVYKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPDENDDVVYKIT 540
Qy 541 GHFYACQVAORAKIOELITGVKHOQKALOSGPPSRRK 579
Db 541 GHFYACQVAORAKIOELITGVKHOQKALOSGPPSRRK 579

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## RESULT 4

```

ID ABB74997 standard; Protein; 579 AA.
AC ABB74997;
DT 01-MAY-2002 (first entry)
XX Human lung tumour L523S protein sequence SEQ ID NO:348.
DE Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX Homo sapiens.
OS Homo sapiens.
PM W0200200174-A2.
PD 03-JAN-2002.
XX 28-JUN-2001; 2001MO-US21065.
PR 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643787.
PR 13-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.

```

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PR 07-MAY-2001; 2001US-0850716.
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnierakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR MPI: 2002-090513/12.
DR N-PSDB: ABL49254.
XX
PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
PS Example 2; Page 330-332; 374pp: English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 579 AA;

```

```

Query Match      65.1%; Score 377; DB 23; Length 579;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIENALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIENALSGK 60
QY 61 IELHGPRIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVQGVGVESECEQVNDSETA 120
DB 61 IELHGPRIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVQGVGVESECEQVNDSETA 120
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOONPLQOPRGRKGLQGRSS 180
DB 121 VVNVYSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOONPLQOPRGRKGLQGRSS 180
QY 181 ROGSPGVSQKPCDPLRLVPTQFVGAIIGKSGATIRNITQOSKIDVHRKEMAGAA 240
DB 181 ROGSPGVSQKPCDPLRLVPTQFVGAIIGKSGATIRNITQOSKIDVHRKEMAGAA 240
QY 241 EKSTILSTPGTSAACKSTILEIMHKEADIKFTEELPLKILAHNNFVGRIGREGRNLK 300
DB 241 EKSTILSTPGTSAACKSTILEIMHKEADIKFTEELPLKILAHNNFVGRIGREGRNLK 300
QY 301 KIEODTTRITISPLQELTLYNPERTITVKNVETKAKAEELMKKIRESYENDIASMNL 360
DB 301 KIEODTTRITISPLQELTLYNPERTITVKNVETKAKAEELMKKIRESYENDIASMNL 360
QY 361 QAHLLIPGLNALGLPPTSGMPPTSGPPSAMTPPYPOEOSTETVHQETPALSGAI 420
DB 361 QAHLLIPGLNALGLPPTSGMPPTSGPPSAMTPPYPOEOSTETVHQETPALSGAI 420
QY 421 IKGGOHITKOLSRFAGASIKIAFAEPDAKVRVYIITGPEAOFKAGKIGKIKENFV 480
DB 421 IKGGOHITKOLSRFAGASIKIAFAEPDAKVRVYIITGPEAOFKAGKIGKIKENFV 480
QY 481 SPEEYKLEAHIRVPSFAAGRVIGKGTIVNELONLSAEVAVVPDRDPTDENDVAVKIT 540
DB 481 SPEEYKLEAHIRVPSFAAGRVIGKGTIVNELONLSAEVAVVPDRDPTDENDVAVKIT 540
QY 541 GHEYACQVAORRIGIELITVQKCHQOQKALQSGPPSSRRK 579
DB 541 GHEYACQVAORRIGIELITVQKCHQOQKALQSGPPSSRRK 579

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RESULT 5
ABR75053
XX ABR75053 standard; Protein: 579 AA.
XX
AC ABR75053;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human lung tumour L523S recombinant protein sequence SEQ ID NO:446.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX immune response.
XX
OS Homo sapiens.
XX
PN WO200200174-A2.
XX
PD 03-JAN-2002.
XX
PE 28-JUN-2001; 2001WO-US21065.
XX
PF 28-JUN-2000; 2000US-0606421.
XX
PR 02-AUG-2000; 2000US-0630940.
XX
PR 21-AUG-2000; 2000US-0643597.
XX
PR 15-SEP-2000; 2000US-0662786.
XX
PR 09-OCT-2000; 2000US-0685696.
XX
PR 12-DEC-2000; 2000US-0735705.
XX
PR 07-MAY-2001; 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnierakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR MPI: 2002-090513/12.
DR N-PSDB: ABL49297.
XX
PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
PS Claim 2; Page 365-367; 374pp: English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 579 AA;

```

```

Query Match      65.1%; Score 377; DB 23; Length 579;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIENALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIENALSGK 60
QY 61 IELHGPRIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVQGVGVESECEQVNDSETA 120
DB 61 IELHGPRIEVEHSVPRKORIRKLOIRNIPHLQMEVLDLSLVQGVGVESECEQVNDSETA 120
QY 121 VVNVYSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOONPLQOPRGRKGLQGRSS 180
DB 121 VVNVYSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOONPLQOPRGRKGLQGRSS 180
QY 181 ROGSPGVSQKPCDPLRLVPTQFVGAIIGKSGATIRNITQOSKIDVHRKEMAGAA 240
DB 181 ROGSPGVSQKPCDPLRLVPTQFVGAIIGKSGATIRNITQOSKIDVHRKEMAGAA 240

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Db 181 RQSPGVSVKQKPCDPLRLVLPVGFVGAIIIGKGAIRINIKTQOSKIDVHRKENAGAA 240  
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 Db 241 EKSTIIISPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNVGRIGKEGRNLK 300  
 QY 301 KIEODDTKTTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESENDIASMNL 360  
 Db 301 KIEODDTKTTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESENDIASMNL 360  
 QY 361 QAHLIPGLNINLALGLFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 Db 361 QAHLIPGLNINLALGLFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 QY 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVRVNIITGPPEAOFKAAGRILYGIKEENFV 480  
 Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVRVNIITGPPEAOFKAAGRILYGIKEENFV 480  
 QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELONLSSAEVVPDPTPDENDQVVKIT 540  
 Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELONLSSAEVVPDPTPDENDQVVKIT 540  
 QY 541 GHFYACOVAQRKIOEILTVYKHQOQKALQSGPPQSRK 579  
 Db 541 GHFYACOVAQRKIOEILTVYKHQOQKALQSGPPQSRK 579

## RESULT 6

ID ABB75054 standard; Protein; 579 AA.  
 XX ABB75054;

AC ABB75054;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L523s recombinant protein sequence SEQ ID NO:449.

KW Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KM Immune response.

OS Homo sapiens.

PN WO200200174-A2.

PD 03-JAN-2002.

PF 28-JUN-2001; 2001WO-US21065.

PR 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

DR MPI: 2002-090513/12.

DR N-PSDB; ABL49299.

PS Claim 2; page 368-369; 374pp; English.

CC The present invention describes human lung tumour proteins. Human lung  
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumour proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB7946 to  
 CC ABB75070 represent sequences used in the exemplification of the present  
 CC invention.

SO Sequence 579 AA;

Query Match 65.1%; Score 377; DB 23; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLTIGNLSENAPSDLESIFKDAKIPVSGPFLVKGVAFVDCPDSSMLKATEALSGK 60  
 Db 1 MNKLTIGNLSENAPSDLESIFKDAKIPVSGPFLVKGVAFVDCPDSSMLKATEALSGK 60  
 QY 61 IELHGKPIEVEHVSYPKRQRIKLIQIRNIPHLQWEVLDSLVOYGVESEQVNTDSETA 120  
 Db 61 IELHGKPIEVEHVSYPKRQRIKLIQIRNIPHLQWEVLDSLVOYGVESEQVNTDSETA 120  
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 Db 121 VVNVTVSSKQOARQALDKNGFQLENTTLKVAIIPDETAQONPLOOPRGRRIGQGGSS 180  
 QY 181 RQSPGVSVKQKPCDPLRLVLPVGFVGAIIIGKGAIRINIKTQOSKIDVHRKENAGAA 240  
 Db 181 RQSPGVSVKQKPCDPLRLVLPVGFVGAIIIGKGAIRINIKTQOSKIDVHRKENAGAA 240  
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 Db 241 EKSTIIISPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNVGRIGKEGRNLK 300  
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 Db 301 KIEODDTKTTISPLQELTYNPERTITVKGNETCAKAEELMKKIRESENDIASMNL 360  
 QY 361 QAHLIPGLNINLALGLFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
 Db 361 QAHLIPGLNINLALGLFPPTSGMPPTSGPPSAMTPPYPOFQSETEVHOFIPALSGAI 420  
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 Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVRVNIITGPPEAOFKAAGRILYGIKEENFV 480  
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 Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTYNELONLSSAEVVPDPTPDENDQVVKIT 540  
 QY 541 GHFYACOVAQRKIOEILTVYKHQOQKALQSGPPQSRK 579  
 Db 541 GHFYACOVAQRKIOEILTVYKHQOQKALQSGPPQSRK 579

## RESULT 7

ID ABB75048 standard; Protein; 586 AA.  
 XX ABB75048;

AC ABB75048;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L523s recombinant protein sequence SEQ ID NO:427.

KW Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KM Immune response.

OS Homo sapiens.

PN WO200200174-A2.

PD 03-JAN-2002.

PF 28-JUN-2001; 2001WO-US21065.  
 XX 28-JUN-2000; 2000US-0606421.  
 PR 02-AUG-2000; 2000US-0630940.  
 PR 21-AUG-2000; 2000US-0643597.  
 PR 15-SEP-2000; 2000US-0662786.  
 PR 09-OCT-2000; 2000US-0685696.  
 PR 12-DEC-2000; 2000US-0735705.  
 PR 07-MAY-2001; 2001US-0850716.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retter MW, Marnierals M, Fanger GR;  
 PI Vedvyck JS, Carter D, Watanabe Y, Peckham DW;  
 DR WPI: 2002-090513/12.  
 DR N-PSDB: ABL49283.  
 XX  
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
 PT lung cancer or stimulating an immune response -  
 PS  
 PS Claim 2; Page 354-355; 374pp; English.  
 XX  
 CC The present invention describes human lung tumour proteins, human lung  
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production, compositions  
 CC comprising the lung tumour proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumour proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL48959 to ABL49300 and ABL4946 to  
 CC ABL495070 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SO Sequence 586 AA;  
 Query Match 64.9%; Score 376; DB 23; Length 586;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 NKLTYGNLSNNAAPSDLESIFKDAKIPVSGPELVYTGAFVDCDESNALKAIEALSGKT 61  
 DB 9 NKLTYGNLSNNAAPSDLESIFKDAKIPVSGPELVYTGAFVDCDESNALKAIEALSGKT 68  
 QY 62 ELHGKPIREHSEVPRKRIKRLQIRNIPHLQMEVLDLSLYQGVGVESCEQVNDSEFAY 121  
 DB 69 ELHGKPIREHSEVPRKRIKRLQIRNIPHLQMEVLDLSLYQGVGVESCEQVNDSEFAY 128  
 QY 122 VAVYSSKDOARQALDLKNGFOLNFTLKVAYITPDMMAOONPILOPRGRGIGOGSSR 181  
 DB 129 VAVYSSKDOARQALDLKNGFOLNFTLKVAYITPDMMAOONPILOPRGRGIGOGSSR 188  
 QY 182 GOSPGSVKOKPCDPLRLVLPPOFGAIEGEGATINIKOTQSKIDVHKENAGAAE 241  
 DB 189 GOSPGSVKOKPCDPLRLVLPPOFGAIEGEGATINIKOTQSKIDVHKENAGAAE 248  
 QY 242 KSITLSTPEBSTSAACKSILEIMHKAQODIKTEEIPKILAHNNFVGRLLIGEGNNLK 301  
 DB 249 KSITLSTPEBSTSAACKSILEIMHKAQODIKTEEIPKILAHNNFVGRLLIGEGNNLK 308  
 QY 302 IEODTDKITITISPLQELTLNPERITTVKGVNETCAKEEIMKIRESEYENDIASMNQ 361  
 DB 309 IEODTDKITITISPLQELTLNPERITTVKGVNETCAKEEIMKIRESEYENDIASMNQ 368  
 QY 362 AHLIPGLNLNLGLFPTSGMPPTSGPSAMTPYPOFQESSETYVHOFIPLASGATII 421  
 DB 369 AHLIPGLNLNLGLFPTSGMPPTSGPSAMTPYPOFQESSETYVHOFIPLASGATII 428  
 QY 422 GKOGCHIKOLSRFAGASIKTAPEADAKVNRVYITGPEEAKFQAQGRITGKIEENFVS 481  
 DB 429 GKOGCHIKOLSRFAGASIKTAPEADAKVNRVYITGPEEAKFQAQGRITGKIEENFVS 488  
 QY 482 PKEEVKLEAHIRVPSFAAGVIGKGGKTVNELONLSAEEVAVVPDQTPDENDDVAVKING 541

DB 489 PKEEVKLEAHIRVPSFAAGVIGKGGKTVNELONLSAEEVAVVPDQTPDENDDVAVKING 548  
 QY 542 HFFACQVAKRKIQEITLVYKCHQOQKALQSGPPQSRK 579  
 DB 549 HFFACQVAKRKIQEITLVYKCHQOQKALQSGPPQSRK 586  
 RESULT 8  
 ID ABG21963 standard; Protein; 619 AA.  
 AC ABG21963;  
 DT 18-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #21954.  
 XX  
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PE 30-MAR-2001; 2001WO-US08631.  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Drmanac RT, Liu C, Tang YT;  
 PI  
 DR WPI: 2001-639362/73.  
 DR N-PSDB: AAS86150.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 PS  
 PS Claim 20; SEQ ID NO 52322; 103pp; English.  
 CC  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations in  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SO Sequence 619 AA;  
 Query Match 25.7%; Score 149; DB 22; Length 619;  
 Best Local Similarity 100.0%; Pred. No. 5e-143;  
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 STEEGTSACKSILEIMKREADIKFTTEIPKTLAHNNVGLICREGRNKRIEODTD 307  
 DB 288 STEEGTSACKSILEIMKREADIKFTTEIPKTLAHNNVGLICREGRNKRIEODTD 347  
 QY 308 TKTITSPLOELTYLPNERTITVKGNETCAKAEKEIMKRIRESYENDIASMNLQAHLLPG 367  
 DB 348 TKTITSPLOELTYLPNERTITVKGNETCAKAEKEIMKRIRESYENDIASMNLQAHLLPG 407  
 QY 368 LNLNAGLFPPTSGMPPTSGPPSAMMP 396  
 DB 408 LNLNAGLFPPTSGMPPTSGPPSAMMP 436

RESULT 9  
 ABG21962 ID ABG21962 standard; Protein; 148 AA.  
 XX  
 AC ABG21962;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #21953.  
 XX  
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PE 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 DR WPI: 2001-639362/73.  
 DR N-PSDB: AAS86149.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 XX  
 PS Claim 20; SEQ ID No 52321; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (II) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SQ Sequence 148 AA;  
 Query Match 17.1%; Score 99; DB 22; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-92;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 FIPALSVGAIGKGGQHIKOLSRFAGASIKIAPAEAPDAKYRMVITTPPEACFKAGRI 470  
 DB 11 FIPALSVGAIGKGGQHIKOLSRFAGASIKIAPAEAPDAKYRMVITTPPEACFKAGRI 70

QY 471 YGKIKENFVSFKREVKLEAHIRVPSFAGRYIGKGT 509  
 DB 71 YGKIKENFVSFKREVKLEAHIRVPSFAGRYIGKGT 109

RESULT 10  
 AAM78238 ID AAM78238 standard; Protein; 93 AA.  
 XX  
 AC AAM78238;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38544.  
 XX  
 KW Human: bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157276-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PE 30-JAN-2001; 2001WO-US00668.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI: 2001-488900/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4; SEQ ID NO: 38544; 658bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.  
 XX  
 SQ Sequence 93 AA;  
 Query Match 16.1%; Score 93; DB 22; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-86;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 ALDKINGFQLNFTLTKVAYIPDEMAAQNPLOQPRGRGICGSGSSRGSPGVSXKQPC 194  
 DB 1 ALDKINGFQLNFTLTKVAYIPDEMAAQNPLOQPRGRGICGSGSSRGSPGVSXKQPC 60

```
OY 195 DLPRLVPTQFVGAIIGKAGATIRNITKOTOS 227
      |||||
DB 61 DLPRLVPTQFVGAIIGKAGATIRNITKOTOS 93

RESULT 11
ID AAM38501 standard; Protein: 93 AA.
XX
XX AAM38501;
AC
XX 17-OCT-2001 (first entry)
DT
XX
DE Peptide #12538 encoded by probe for measuring placental gene expression.
XX
XX Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200157272-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00663.
PP
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488897/53.
DR
XX
XX WPI; 2001-488897/53.
PT
XX Human genome-derived single exon nucleic acid probes useful for
PS analyzing gene expression in human placenta.
PS Claim 27; SEQ ID No 38770; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
CC
XX
XX Sequence 93 AA:
SQ
Query Match 16.18; Score 93; DB 22; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 135 ALDKNGFQLENTIKAVIYIDEMAQONPQQPGRGICQKSSSQSGPSVSKQPC 194
      |||||
DB 1 ALDKNGFQLENTIKAVIYIDEMAQONPQQPGRGICQKSSSQSGPSVSKQPC 60
OY 195 DLPRLVPTQFVGAIIGKAGATIRNITKOTOS 227
      |||||
DB 61 DLPRLVPTQFVGAIIGKAGATIRNITKOTOS 93

RESULT 12
ABG12592
ID ABG12592 standard; Protein: 583 AA.
XX
XX ABG12592;
XX

PT 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #12583.
DE
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensics;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US08631.
PP
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR
XX N-PSDB; AAS76779.
DR
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID No 42951; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations in
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 583 AA:
SQ
Query Match 11.2%; Score 65; DB 22; Length 583;
Best Local Similarity 100.0%; Pred. No. 3e-57;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 LVVPTQFVGAIIGKAGATIRNITKOTOSKIDVHKKENAGAAEKSTIIISTEGTSACKS 259
      |||||
DB 204 LVVPTQFVGAIIGKAGATIRNITKOTOSKIDVHKKENAGAAEKSTIIISTEGTSACKS 263
OY 260 ILEIM 264
      |||||
DB 264 ILEIM 268

RESULT 13
ABB43427
ID ABB43427 standard; Peptide: 45 AA.
XX
XX ABB43427;
XX
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AC  ABB43427;
XX
PD  04-FEB-2002 (first entry)
XX
DE  Peptide #10933 encoded by human foetal liver single exon probe.
XX
KW  Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS  Homo sapiens.
XX
PN  WO200157277-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US00669.
XX
PR  04-FEB-2000; 2000US-0180312.
XX
PR  26-MAY-2000; 2000US-0207456.
XX
PR  30-JUN-2000; 2000US-0608408.
XX
PR  03-AUG-2000; 2000US-0632366.
XX
PR  21-SEP-2000; 2000US-0234687.
XX
PR  27-SEP-2000; 2000US-0236359.
XX
PR  04-OCT-2000; 2000GB-0024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-483447/52.
XX
PT  Human genome-derived single exon nucleic acid probes useful for
XX
PT  analyzing gene expression in human fetal liver -
XX
PS  Claim 27; SEQ ID NO 36062; 639pp + sequence listing; English.
XX
XX  The invention relates to a single exon nucleic acid probe for
XX  measuring human gene expression in a sample derived from human foetal
XX  liver. The single exon nucleic acid probes may be used for predicting,
XX  measuring and displaying gene expression in samples derived from human
XX  fetal liver. The present sequence is a peptide encoded by a single exon
XX  nucleic acid probe of the invention.
XX  Note: The sequence data for this patent did not form part of the
XX  printed specification, but was obtained in electronic format directly
XX  from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ  Sequence 45 AA;

Query Match 7.8%; Score 45; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  315 LOELTYLPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 359
DB  1 LOELTYLPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 45

RESULT 14
ID  AAM64356
XX  AAM64356 standard; Protein; 45 AA.
XX
AC  AAM64356;
XX
DT  05-NOV-2001 (first entry)
XX
DE  Human brain expressed single exon probe encoded protein SEQ ID NO: 36461.
XX
XX  Human; brain expressed exon; gene expression analysis; probe;
XX  microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX  epilepsy; cancer.
XX
OS  Homo sapiens.
XX
PN  WO200157275-A2.

```

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XX
PD  09-AUG-2001.
XX
DE  30-JAN-2001; 2001WO-US00667.
XX
PF  04-FEB-2000; 2000US-0180312.
XX
PR  26-MAY-2000; 2000US-0207456.
XX
PR  30-JUN-2000; 2000US-0608408.
XX
PR  03-AUG-2000; 2000US-0632366.
XX
PR  21-SEP-2000; 2000US-0234687.
XX
PR  27-SEP-2000; 2000US-0236359.
XX
PR  04-OCT-2000; 2000GB-0024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-483446/52.
XX
PT  Single exon nucleic acid probes for analyzing gene expression in human
XX
PT  brains -
XX
PS  Example 4; SEQ ID NO: 36461; 650pp + Sequence listing; English.
XX
XX  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
XX  brain. They can be used to measure gene expression in brain cell samples,
XX  which may enable the diagnosis and improved treatment of nervous system
XX  diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX  epilepsy and cancers. The present sequence is a protein encoded by one of
XX  the probes of the invention.
XX
SQ  Sequence 45 AA;

Query Match 7.8%; Score 45; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  315 LOELTYLPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 359
DB  1 LOELTYLPERTTYKGNVETCAKAEIEIMKKIRSEYENDIASMN 45

RESULT 15
ID  AAM37315
XX  AAM37315 standard; Protein; 45 AA.
XX
AC  AAM37315;
XX
DT  17-OCT-2001 (first entry)
XX
DE  Peptide #11352 encoded by probe for measuring placental gene expression.
XX
XX  Probe; microarray; human; placenta; antenatal diagnosis;
XX  genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200157272-A2.
XX
DT  09-AUG-2001.
XX
DE  30-JAN-2001; 2001WO-US00663.
XX
PR  04-FEB-2000; 2000US-0180312.
XX
PR  26-MAY-2000; 2000US-0207456.
XX
PR  30-JUN-2000; 2000US-0608408.
XX
PR  03-AUG-2000; 2000US-0632366.
XX
PR  21-SEP-2000; 2000US-0234687.
XX
PR  27-SEP-2000; 2000US-0236359.
XX
PR  04-OCT-2000; 2000GB-0024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.

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Page 10

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XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-48897/53.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 27: SEQ ID No 37584; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
XX see A113135-A1157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders.
XX
XX Sequence 45 AA:
SQ
Query Match 7.8%; Score 45; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 315 LQELTYNPERTITVKGAVETCAKAEIEIMKTIRESYENDIASMN 359
DB 1 LQELTYNPERTITVKGAVETCAKAEIEIMKTIRESYENDIASMN 45
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Job time : 134.103 secs

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:32:15 ; Search time 40.8818 Seconds  
(without alignments)  
416.711 Million cell updates/sec

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Title: US-09-897-778-176
Perfect score: 579
Sequence: 1 MNKLVIGNLSENAPSDLES.....YKQHQQKALQSGPPQSRK 579

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Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

Database :

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3:  /cgn2_6/plodata1/laa/5B.COMB.pcp:*
4:  /cgn2_6/plodata1/laa/6A.COMB.pcp:*
5:  /cgn2_6/plodata1/laa/6B.COMB.pcp:*
6:  /cgn2_6/plodata1/laa/PCrTOS.COMB.pcp:*
7:  /cgn2_6/plodata1/laa/backfiles1.pcp:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	579	100.0	579	4	US-09-643-597-176	Sequence 1/6, App
2	377	65.1	579	4	US-09-643-597-348	Sequence 3/4, App
3	48	8.3	48	4	US-09-261-855-24	Sequence 21, App
4	47	8.1	47	4	US-09-261-855-23	Sequence 23, App
5	42	7.3	49	4	US-09-261-855-22	Sequence 17, App
6	36	6.2	47	4	US-09-261-855-17	Sequence 12, App
7	36	6.2	577	4	US-09-261-855-2	Sequence 2, App
8	21	5.5	47	4	US-09-261-855-21	Sequence 21, App
9	21	5.5	49	4	US-09-261-855-18	Sequence 18, App
10	9	3.3	48	4	US-09-261-855-20	Sequence 20, App
11	14	2.4	14	4	US-09-261-855-4	Sequence 4, App
12	11	1.9	11	4	US-09-261-855-11	Sequence 11, App
13	11	1.9	11	4	US-09-261-855-14	Sequence 14, App
14	11	1.9	47	4	US-09-261-855-19	Sequence 19, App
15	11	1.4	11	4	US-09-261-855-10	Sequence 10, App
16	8	1.4	1375	3	US-08-665-259-26	Sequence 26, App
17	8	1.4	1375	3	US-08-762-500-26	Sequence 26, App
18	8	1.4	1457	3	US-08-665-259-27	Sequence 27, App
19	8	1.4	1457	3	US-08-762-500-27	Sequence 27, App
20	8	1.4	1684	3	US-08-665-259-25	Sequence 25, App
21	8	1.4	1684	3	US-08-762-500-25	Sequence 25, App
22	8	1.4	1704	3	US-08-762-500-75	Sequence 75, App
23	8	1.4	9	2	US-08-340-283-11	Sequence 11, App
24	7	1.2	35	4	US-08-722-015A-324	Sequence 224, App
25	7	1.2	50	4	US-09-261-855-25	Sequence 25, App
26	7	1.2	67	4	US-08-986-856B-17	Sequence 17, App
27	7	1.2	74	4	US-08-469-260A-498	Sequence 498, App

28	1.68	2	US-08-612-788-77	Sequence 27, Appl
29	1.62	3	US-09-066-028-77	Sequence 27, Appl
30	1.81	4	US-09-134-001C-4852	Sequence 4852, Appl
31	1.2	2	US-08-612-788-82	Sequence 32, Appl
32	2.50	3	US-09-066-028-82	Sequence 32, Appl
33	2.99	4	US-08-879-098-2	Sequence 2, Appl
34	2.99	4	US-09-631-548-2	Sequence 2, Appl
35	3.12	4	US-09-134-001C-3668	Sequence 3668, Appl
36	1.2	3	US-08-248-629A-5	Sequence 5, Appl
37	3.39	1	US-08-451-932-5	Sequence 5, Appl
38	3.39	1	US-08-452-260-5	Sequence 5, Appl
39	1.2	3	US-08-326-785-5	Sequence 5, Appl
40	3.39	1	US-08-612-788-5	Sequence 5, Appl
41	1.2	3	US-08-612-788-5	Sequence 5, Appl
42	3.39	2	US-08-629-598B-5	Sequence 5, Appl
43	3.39	2	US-08-429-743-5	Sequence 5, Appl
44	3.39	2	US-08-866-735-5	Sequence 5, Appl
45	3.39	5	US-09-066-028-5	Sequence 5, Appl
			PCT-US93-05107-5	Sequence 5, Appl

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RESULT 1
US-09-643-597-176
? Sequence 176, Application US/09643597
? Patent No. 6426072
GENERAL INFORMATION:
? APPLICANT: Wang, Tongtong
? APPLICANT: Pan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aijun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY OF LUNG CANCER
? FILE REFERENCE: 210121.455C11
? CURRENT APPLICATION NUMBER: US/09/643,597
? CURRENT FILING DATE: 2000-08-21
? NUMBER OF SEQ. ID NOS.: 369
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ. ID NO. 176
? LENGTH: 579
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-643-597-176

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Query Match	100.0%;	Score 579;	DB 4;	Length 579;
Best local Similarity	100.0%;	Pred. No. 0;		
Matches 579; Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	

QY	1	MNKLTYGNLSENAA	SDSEJFPIKAKPI	IVSPPELVTKGYFVVC	PPESNAAIKATIAL	SGK	60
Db	1	MNKLTYGNLSENAA	SDSEJFPIKAKPI	IVSPPELVTKGYFVVC	PPESNAAIKATIAL	SGK	60
QY	61	IELHGPRIEVHSVPR	KROKIRKLOIRNI	PHLOWEVLDSLLV	GYGVESCEQVMTDSE	TA	120
Db	61	IELHGPRIEVHSVPR	KROKIRKLOIRNI	PHLOWEVLDSLLV	GYGVESCEQVMTDSE	TA	120
QY	61	IELHGPRIEVHSVPR	KROKIRKLOIRNI	PHLOWEVLDSLLV	GYGVESCEQVMTDSE	TA	120
Db	61	IELHGPRIEVHSVPR	KROKIRKLOIRNI	PHLOWEVLDSLLV	GYGVESCEQVMTDSE	TA	120
QY	121	VVAVVYSSSDQARQ	ALDLKINGFOLENT	FLKAYIIPDEMAQ	QNPLODQPRGRGLDQ	RSSS	180
Db	121	VVAVVYSSSDQARQ	ALDLKINGFOLENT	FLKAYIIPDEMAQ	QNPLODQPRGRGLDQ	RSSS	180
QY	181	RQSPSPSVSKORPC	DLPLRLVPTQFVGA	IGEGATIRINIRKQ	OTQSDIVJIRKENA	GA	240
Db	181	RQSPSPSVSKORPC	DLPLRLVPTQFVGA	IGEGATIRINIRKQ	OTQSDIVJIRKENA	GA	240
QY	241	EKSITTLSTPEGT	SAACKSILEIMHKE	ADIKFTBEIPLKILAH	NNVGRGLGEGRMLK		
Db	241	EKSITTLSTPEGT	SAACKSILEIMHKE	ADIKFTBEIPLKILAH	NNVGRGLGEGRMLK		

Thu Apr 17 07:55:17 2003

us-09-897-778-176.Oligo.ra1

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Db 241 EKSTITLSTPEGTSAAKSIILEIMHKEADODIKFTEELPLKILANNFVGRILKEGRNLK 300
OY 301 KIEDDTTKITISPLQELTLNPERTITVKGWNETCAKAEELIMKIRESEYENDIASMNL 360
Db 301 KIEDDTTKITISPLQELTLNPERTITVKGWNETCAKAEELIMKIRESEYENDIASMNL 360
OY 361 QAHLIPGLNALGLPPTSGMPPTSGPPSANTPEYQFQDSETEVHOFIPALSVGAI 420
Db 361 QAHLIPGLNALGLPPTSGMPPTSGPPSANTPEYQFQDSETEVHOFIPALSVGAI 420
OY 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVNRVYITGPEAOFKAGRIYGIKEENFV 480
Db 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVNRVYITGPEAOFKAGRIYGIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELQNLSSAEVVPDQTPDENDOVVYKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELQNLSSAEVVPDQTPDENDOVVYKIT 540
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Db 541 GHFYACOVAORRKIOELITOVKHOQKALQSGPPQSRK 579
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RESULT 2
US-09-643-597-348
Sequence 348, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: Fasted for Windows Version 3.0
SEQ LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-348
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Best Local Similarity 98.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 MNKLYGNLSMAAPSDLESIFPDAKIPYSGPVLKCYAPVNCDEPESALKATLEALSCK 60
OY 61 IELHGKPILEVHSPKRRIRKIOINIPHIOWEVIDSLLOYGVESCEQVWMDSETA 120
Db 61 IELHGKPILEVHSPKRRIRKIOINIPHIOWEVIDSLLOYGVESCEQVWMDSETA 120
OY 121 VVWVYSSKDAORALDKNGFQLENFTLKVAYIPDEMAAQQPFLQOPGRGGLGQSSS 180
Db 121 VVWVYSSKDAORALDKNGFQLENFTLKVAYIPDEMAAQQPFLQOPGRGGLGQSSS 180
OY 181 ROGSPGVSVKOPDOLPLRLIVPTQFVGALIGKEGATIRNTQOTQSKIDVHRKMGAA 240
Db 181 ROGSPGVSVKOPDOLPLRLIVPTQFVGALIGKEGATIRNTQOTQSKIDVHRKMGAA 240
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OY 241 EKSTITLSTPEGTSAAKSIILEIMHKEADODIKFTEELPLKILANNFVGRILKEGRNLK 300
Db 241 EKSTITLSTPEGTSAAKSIILEIMHKEADODIKFTEELPLKILANNFVGRILKEGRNLK 300
OY 301 KIEDDTTKITISPLQELTLNPERTITVKGWNETCAKAEELIMKIRESEYENDIASMNL 360
Db 301 KIEDDTTKITISPLQELTLNPERTITVKGWNETCAKAEELIMKIRESEYENDIASMNL 360
OY 361 QAHLIPGLNALGLPPTSGMPPTSGPPSANTPEYQFQDSETEVHOFIPALSVGAI 420
Db 361 QAHLIPGLNALGLPPTSGMPPTSGPPSANTPEYQFQDSETEVHOFIPALSVGAI 420
OY 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVNRVYITGPEAOFKAGRIYGIKEENFV 480
Db 421 IKGQGHIKOLSRFAGASIKIAPAEADAKVNRVYITGPEAOFKAGRIYGIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELQNLSSAEVVPDQTPDENDOVVYKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELQNLSSAEVVPDQTPDENDOVVYKIT 540
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Db 541 GHFYACOVAORRKIOELITOVKHOQKALQSGPPQSRK 579
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RESULT 3
US-09-261-855-24
Sequence 24, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CMD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 24
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-24
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Query Match 8.3%; Score 48; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 3; Gaps 0;
Matches 48; Conservative 0; Mismatches 0; Indels 0;
OY 482 IRVPSFAAGRVIGKGTYNELQNLSSAEVVPDQTPDENDOVVYKIT 539
Db 1 IRVPSFAAGRVIGKGTYNELQNLSSAEVVPDQTPDENDOVVYKIT 48
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RESULT 4
US-09-261-855-23
Sequence 23, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CMD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 23
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-23
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Query Match 8.1%; Score 47; DB 4; Length 47;



Best Local Similarity 100.0%; Pred. No. 3.4e-39;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 410 QFIPALSVGALIGKQGHKQSLRFGASIKIPAPAPAKRYMYI 456  
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Db 1 QFIPALSVGALIGKQGHKQSLRFGASIKIPAPAPAKRYMYI 47

RESULT 5  
US-09-261-855-22  
; Sequence 22, Application US/09261855A  
; Patent No. 6255055  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; FILE REFERENCE: 960296.95131  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-261-855-22

Query Match 7.3%; Score 42; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 288 VGRLLGKGRRLKKEEDTPTKITISPLDLYNPERITTV 329  
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Db 8 VGRLLGKGRRLKKEEDTPTKITISPLDLYNPERITTV 49

RESULT 6  
US-09-261-855-17  
; Sequence 17, Application US/09261855A  
; Patent No. 6255055  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; FILE REFERENCE: 960296.95131  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-261-855-17

Query Match 6.2%; Score 36; DB 4; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 207 VGATIGKGGATIRNITKOTOSKIDVHRKKNAGAAEK 242  
|||||  
Db 8 VGATIGKGGATIRNITKOTOSKIDVHRKKNAGAAEK 43

RESULT 7  
US-09-261-855-2  
; Sequence 2, Application US/09261855A  
; Patent No. 6255055  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; FILE REFERENCE: 960296.95131

; CURRENT APPLICATION NUMBER: US/09/261,855A  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 577  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-261-855-2

Query Match 6.2%; Score 36; DB 4; Length 577;  
Best Local Similarity 100.0%; Pred. No. 2.9e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 207 VGATIGKGGATIRNITKOTOSKIDVHRKKNAGAAEK 242  
|||||  
Db 207 VGATIGKGGATIRNITKOTOSKIDVHRKKNAGAAEK 242

RESULT 8  
US-09-261-855-21  
; Sequence 21, Application US/09261855A  
; Patent No. 6255055  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; FILE REFERENCE: 960296.95131  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-261-855-21

Query Match 5.5%; Score 32; DB 4; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 215 GATIRNITKOTOSKIDVHRKKNAGAAEKSTIT 246  
|||||  
Db 16 GATIRNITKOTOSKIDVHRKKNAGAAEKSTIT 47

RESULT 9  
US-09-261-855-18  
; Sequence 18, Application US/09261855A  
; Patent No. 6255055  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; FILE REFERENCE: 960296.95131  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-261-855-18

Query Match 3.6%; Score 21; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.3e-13;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 281 ILAHNNFVGLIGKGRRLK 301  
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Db 1 ILAHNNFVGLIGKGRRLK 21

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Page 4

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RESULT 10
US-09-261-855-20
Sequence 20, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 48
TYPE: PRT
ORGANISM: Mus musculus
US-09-261-855-20

Query Match
Best Local Similarity 3.3%; Score 19; DB 4; Length 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 AAGRVIGKRGKTYNELNL 516
DB 7 AAGRVIGKRGKTYNELNL 25

RESULT 11
US-09-261-855-4
Sequence 4, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-4

Query Match
Best Local Similarity 100.0%; Score 14; DB 4; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GRRGLGGRSSROG 183
DB 1 GRRGLGGRSSROG 14

RESULT 12
US-09-261-855-11
Sequence 11, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 11
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-11

Query Match
Best Local Similarity 1.9%; Score 11; DB 4; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 HLOMEVDSL 101
DB 1 HLOMEVDSL 11

RESULT 13
US-09-261-855-14
Sequence 14, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-855-14

Query Match
Best Local Similarity 1.9%; Score 11; DB 4; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 TISPLQELTLY 321
DB 1 TISPLQELTLY 11

RESULT 14
US-09-261-855-19
Sequence 19, Application US/09261855A
Patent No. 6255055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 47
TYPE: PRT
ORGANISM: Mus musculus
US-09-261-855-19

Query Match
Best Local Similarity 1.9%; Score 11; DB 4; Length 47;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 GQHKQLSRFA 435
DB 16 GQHKQLSRFA 26

RESULT 15
US-09-261-855-10
Sequence 10, Application US/09261855A
Patent No. 6255055
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GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE  
; FILE REFERENCE: 960296.95131  
; CURRENT APPLICATION NUMBER: US/09/261,855A  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-261-855-10

Query Match 1.4%; Score 8; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 94 WEVLDL 101  
|||||||  
DB 4 WEVLDL 11

Search completed: April 16, 2003, 16:38:10  
Job time : 42.8818 secs



GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:36:47 ; Search time 66.5517 Seconds  
(without alignments)  
657.841 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579

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Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubppa/PCR\_NEW\_PUB\_PEP:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB\_PEP:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB\_PEP:\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB\_PEP:\*
- 6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB\_PEP:\*
- 7: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB\_PEP:\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB\_PEP:\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB\_PEP:\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB\_PEP:\*
- 11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB\_PEP:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB\_PEP:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB\_PEP:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB\_PEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	100.0	579	10 US-09-735-705-176	Sequence 176, App
2	579	100.0	579	10 US-09-850-716A-176	Sequence 176, App
3	579	100.0	579	10 US-09-897-778-176	Sequence 176, App
4	377	65.1	579	10 US-09-735-705-348	Sequence 348, App
5	377	65.1	579	10 US-09-850-716A-348	Sequence 348, App
6	377	65.1	579	10 US-09-897-778-348	Sequence 348, App
7	377	65.1	579	10 US-09-897-778-446	Sequence 446, App
8	377	65.1	579	10 US-09-897-778-449	Sequence 449, App
9	376	64.9	586	10 US-09-850-716A-427	Sequence 427, App
10	376	64.9	586	10 US-09-897-778-427	Sequence 427, App
11	93	16.1	93	10 US-09-864-761-46606	Sequence 46606, A
12	48	8.3	48	10 US-09-873-637-24	Sequence 24, App1
13	47	8.1	47	10 US-09-873-637-24	Sequence 24, App1
14	45	7.8	45	10 US-09-864-761-45987	Sequence 45987, A
15	42	7.3	49	10 US-09-873-637-22	Sequence 22, App1
16	36	6.2	47	10 US-09-873-637-17	Sequence 17, App1
17	36	6.2	577	10 US-09-873-637-2	Sequence 2, App1
18	32	5.5	47	10 US-09-873-637-21	Sequence 21, App1
19	24	4.1	261	10 US-09-764-864-1114	Sequence 1114, App

20	21	3.6	49	10	US-09-873-637-18	Sequence 18, App1
21	20	3.5	20	10	US-09-735-705-397	Sequence 397, App
22	20	3.5	20	10	US-09-735-705-398	Sequence 398, App
23	20	3.5	20	10	US-09-735-705-399	Sequence 399, App
24	20	3.5	20	10	US-09-735-705-400	Sequence 400, App
25	20	3.5	20	10	US-09-735-705-401	Sequence 401, App
26	20	3.5	20	10	US-09-735-705-402	Sequence 402, App
27	20	3.5	20	10	US-09-735-705-403	Sequence 403, App
28	20	3.5	20	10	US-09-735-705-404	Sequence 404, App
29	20	3.5	20	10	US-09-735-705-405	Sequence 405, App
30	20	3.5	20	10	US-09-735-705-406	Sequence 406, App
31	20	3.5	20	10	US-09-735-705-409	Sequence 409, App
32	20	3.5	20	10	US-09-735-705-410	Sequence 410, App
33	20	3.5	20	10	US-09-735-705-411	Sequence 411, App
34	20	3.5	20	10	US-09-735-705-412	Sequence 412, App
35	20	3.5	20	10	US-09-735-705-413	Sequence 413, App
36	20	3.5	20	10	US-09-735-705-414	Sequence 414, App
37	20	3.5	20	10	US-09-735-705-415	Sequence 415, App
38	20	3.5	20	10	US-09-735-705-416	Sequence 416, App
39	20	3.5	20	10	US-09-735-705-417	Sequence 417, App
40	20	3.5	20	10	US-09-735-705-418	Sequence 418, App
41	20	3.5	20	10	US-09-735-705-419	Sequence 419, App
42	20	3.5	20	10	US-09-850-716A-397	Sequence 397, App
43	20	3.5	20	10	US-09-850-716A-398	Sequence 398, App
44	20	3.5	20	10	US-09-850-716A-399	Sequence 399, App
45	20	3.5	20	10	US-09-850-716A-400	Sequence 400, App

## ALIGNMENTS

RESULT 1  
US-09-735-705-176  
Sequence 176, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-176  
Query Match 100.0%; Score 579; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNSENAAPSDELSIFKDKIPVSGFLVTKCYAVDDPDSMALKATELSCK 60  
DB 1 MNKLYIGNSENAAPSDELSIFKDKIPVSGFLVTKCYAVDDPDSMALKATELSCK 60  
OY 61 IELHGKPIEVESHVPRKRIKQIRNIPHLQWELVDSLIVQYGVESCEQVNTDSETA 120  
DB 61 IELHGKPIEVESHVPRKRIKQIRNIPHLQWELVDSLIVQYGVESCEQVNTDSETA 120

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QY 121 VVNTYSSKDOARALDKINGFOLNFTLVAYIPDEMAAONPLQOPRGRGLGORGSS 180
DB 121 VVNTYSSKDOARALDKINGFOLNFTLVAYIPDEMAAONPLQOPRGRGLGORGSS 180
QY 181 RQSPGVSVKQKPCDPLRLVPTQFVGAIIGKEGATINITKOTQOSKIDVHRKENAGAA 240
DB 181 RQSPGVSVKQKPCDPLRLVPTQFVGAIIGKEGATINITKOTQOSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPEGSTSACKSILEIMHKEADIKFTEBIPKLAHNNPVRGLIKREGRNLK 300
DB 241 EKSTITLSTPEGSTSACKSILEIMHKEADIKFTEBIPKLAHNNPVRGLIKREGRNLK 300
QY 301 KIEODTDTKITISPIQELTLYNPERTITVKGWNETCAKKEEIMKKIRESYENDIASMNL 360
DB 301 KIEODTDTKITISPIQELTLYNPERTITVKGWNETCAKKEEIMKKIRESYENDIASMNL 360
QY 361 QAHLPGLNLTALGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
DB 361 QAHLPGLNLTALGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVNVITITGPPEAQFPAQGRITGRIKEENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVNVITITGPPEAQFPAQGRITGRIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELONLSAEVYVPRDQTPDENQOYVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELONLSAEVYVPRDQTPDENQOYVVKIT 540
QY 541 GHFYACOVAKRKIOELITLOVYKHOQKALQSGPPQSRK 579
DB 541 GHFYACOVAKRKIOELITLOVYKHOQKALQSGPPQSRK 579

RESULT 2
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kajos, Michael D.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match 100.0%; Score 579; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 EKSTITLSTPEGSTSACKSILEIMHKEADIKFTEBIPKLAHNNPVRGLIKREGRNLK 300
DB 241 EKSTITLSTPEGSTSACKSILEIMHKEADIKFTEBIPKLAHNNPVRGLIKREGRNLK 300
QY 301 KIEODTDTKITISPIQELTLYNPERTITVKGWNETCAKKEEIMKKIRESYENDIASMNL 360
DB 301 KIEODTDTKITISPIQELTLYNPERTITVKGWNETCAKKEEIMKKIRESYENDIASMNL 360
QY 361 QAHLPGLNLTALGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
DB 361 QAHLPGLNLTALGLFPPTSGMPPTSGPSAMTPPYPOFQOSETETVHOPIALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVNVITITGPPEAQFPAQGRITGRIKEENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVNVITITGPPEAQFPAQGRITGRIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELONLSAEVYVPRDQTPDENQOYVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELONLSAEVYVPRDQTPDENQOYVVKIT 540
QY 541 GHFYACOVAKRKIOELITLOVYKHOQKALQSGPPQSRK 579
DB 541 GHFYACOVAKRKIOELITLOVYKHOQKALQSGPPQSRK 579

RESULT 3
US-09-897-778-176
: Sequence 176, Application US/09897778
: Patent No. US2002014713A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedrick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-176

Query Match 100.0%; Score 579; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 EKSTILLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300  
QY 301 KIBODDTPTKITTISPLOELTLYNPERTITVKGNVETCAKAEIEIMKKIRESEYENDIASNML 360  
Db 301 KIBODDTPTKITTISPLOELTLYNPERTITVKGNVETCAKAEIEIMKKIRESEYENDIASNML 360  
QY 361 OAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEOSSETETVHOIFIPALSVGAI 420  
Db 361 OAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEOSSETETVHOIFIPALSVGAI 420  
QY 421 IKGOGHITKOLSRFAGASIKIPAPAPDAKVRMYITGPREPOFAKAGRTYKIKEENFY 480  
Db 421 IKGOGHITKOLSRFAGASIKIPAPAPDAKVRMYITGPREPOFAKAGRTYKIKEENFY 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPENDQVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPENDQVVKIT 540  
QY 541 GHFYACQVAKORKIOELITVYKOHQOQKALOSGPPQSRK 579  
Db 541 GHFYACQVAKORKIOELITVYKOHQOQKALOSGPPQSRK 579

## RESULT 4

US-09-735-705-348  
; Sequence 348, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Pan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-348

Query Match 65.1%; Score 377; DB 10; Length 579;

Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPPDSMALKAIEALSCK 60  
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Db 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVYGVVESCQOVNTDSETA 120  
QY 121 VVNTYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRGIGQGGSS 180  
Db 121 VVNTYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRGIGQGGSS 180  
QY 181 ROGSPGSVSKORPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240  
Db 181 ROGSPGSVSKORPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240

Db 181 ROGSPGSVSKORPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240  
QY 241 EKSTILLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300  
Db 241 EKSTILLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300  
QY 301 KIBODDTPTKITTISPLOELTLYNPERTITVKGNVETCAKAEIEIMKKIRESEYENDIASNML 360  
Db 301 KIBODDTPTKITTISPLOELTLYNPERTITVKGNVETCAKAEIEIMKKIRESEYENDIASNML 360  
QY 361 OAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEOSSETETVHOIFIPALSVGAI 420  
Db 361 OAHILIGLMLNMLGLFPPTSGMPPTSGPPSAMPYPOFEOSSETETVHOIFIPALSVGAI 420  
QY 421 IKGOGHITKOLSRFAGASIKIPAPAPDAKVRMYITGPREPOFAKAGRTYKIKEENFY 480  
Db 421 IKGOGHITKOLSRFAGASIKIPAPAPDAKVRMYITGPREPOFAKAGRTYKIKEENFY 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPENDQVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVPBDQTPENDQVVKIT 540  
QY 541 GHFYACQVAKORKIOELITVYKOHQOQKALOSGPPQSRK 579  
Db 541 GHFYACQVAKORKIOELITVYKOHQOQKALOSGPPQSRK 579

## RESULT 5

US-09-850-716A-348  
; Sequence 348, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Rafter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-348

Query Match 65.1%; Score 377; DB 10; Length 579;

Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPPDSMALKAIEALSCK 60  
Db 1 MNKLYIGLNLSENAPSDLESIFPKDAKIPVSGPFLVKTGYAFVDCPPDSMALKAIEALSCK 60  
QY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVYGVVESCQOVNTDSETA 120  
Db 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVYGVVESCQOVNTDSETA 120  
QY 121 VVNTYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRGIGQGGSS 180  
Db 121 VVNTYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQOPRGRRGIGQGGSS 180  
QY 181 ROGSPGSVSKORPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240  
Db 181 ROGSPGSVSKORPCDPLRLVPTQFVGALIGKEGATIRNITKOTOSKIDVHRKENAGAA 240  
QY 241 EKSTILLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300  
Db 241 EKSTILLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300  
QY 301 KIBODDTPTKITTISPLOELTLYNPERTITVKGNVETCAKAEIEIMKKIRESEYENDIASNML 360  
Db 301 KIBODDTPTKITTISPLOELTLYNPERTITVKGNVETCAKAEIEIMKKIRESEYENDIASNML 360

Db 301 KIEODTDTKITISPLQDELTYNPERTIVKGNVETCAKAEELIMKIRISTENDIASNL 360  
QY 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
Db 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
QY 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYVITITGPEAOFAOGRTYKIKENFV 480  
Db 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYVITITGPEAOFAOGRTYKIKENFV 480  
QY 481 SPEEYKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQOTPDENDOVYKIT 540  
Db 481 SPEEYKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQOTPDENDOVYKIT 540  
QY 541 GHEVACQVAKRKIOEILITVYKQHOOQKALOSGPPQSRK 579  
Db 541 GHEVACQVAKRKIOEILITVYKQHOOQKALOSGPPQSRK 579

RESULT 6  
US-09-897-778-348  
Sequence 348, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455016  
CURRENT FILING DATE: US/09/897.778  
CURRENT APPLICATION NUMBER: US/09-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-348

Query Match 65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
QY 61 IELHGKPIEVEHSPKROIRKLOIRNIPHLQWEVDLSLVOYGVESECEQVNDSETA 120  
Db 61 IELHGKPIEVEHSPKROIRKLOIRNIPHLQWEVDLSLVOYGVESECEQVNDSETA 120  
QY 121 VVNYTSSKDDARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPPGRGGLGGRSS 180  
Db 121 VVNYTSSKDDARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPPGRGGLGGRSS 180  
QY 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIIGKGGATIRNITKQNSKIDVHREMGAA 240  
Db 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIIGKGGATIRNITKQNSKIDVHREMGAA 240  
QY 241 EKSTIIISTPEGSTSACKSILEIMKEKODIKFTEELPKILAHNNFVGRGLGEGRNK 300  
Db 241 EKSTIIISTPEGSTSACKSILEIMKEKODIKFTEELPKILAHNNFVGRGLGEGRNK 300  
QY 301 KIEODTDTKITISPLQDELTYNPERTIVKGNVETCAKAEELIMKIRISTENDIASNL 360  
Db 301 KIEODTDTKITISPLQDELTYNPERTIVKGNVETCAKAEELIMKIRISTENDIASNL 360

Db 301 KIEODTDTKITISPLQDELTYNPERTIVKGNVETCAKAEELIMKIRISTENDIASNL 360  
QY 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
Db 361 QAHILPGINLALGLPPTSGMPPTSGPPSAMPPPOPEOSEETVYQFIPALSGAI 420  
QY 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYVITITGPEAOFAOGRTYKIKENFV 480  
Db 421 IKOGQHITKOLSRFAGASIKIAPAEAPDAKRYVITITGPEAOFAOGRTYKIKENFV 480  
QY 481 SPEEYKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQOTPDENDOVYKIT 540  
Db 481 SPEEYKLEAHIRVPSFAAGRYIGKGTVELONLSSAEVVPDQOTPDENDOVYKIT 540  
QY 541 GHEVACQVAKRKIOEILITVYKQHOOQKALOSGPPQSRK 579  
Db 541 GHEVACQVAKRKIOEILITVYKQHOOQKALOSGPPQSRK 579

RESULT 7  
US-09-897-778-446  
Sequence 446, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455016  
CURRENT FILING DATE: US/09/897.778  
CURRENT APPLICATION NUMBER: US/09-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 446  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-446

Query Match 65.1%; Score 377; DB 10; Length 579;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKATEALSCK 60  
QY 61 IELHGKPIEVEHSPKROIRKLOIRNIPHLQWEVDLSLVOYGVESECEQVNDSETA 120  
Db 61 IELHGKPIEVEHSPKROIRKLOIRNIPHLQWEVDLSLVOYGVESECEQVNDSETA 120  
QY 121 VVNYTSSKDDARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPPGRGGLGGRSS 180  
Db 121 VVNYTSSKDDARQALDKLNGFOLNFTLKVAIYIPDEMAOQNPLOQPPGRGGLGGRSS 180  
QY 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIIGKGGATIRNITKQNSKIDVHREMGAA 240  
Db 181 RGSFGSVSKOKPCDPLRLRLVPTQFVGAIIIGKGGATIRNITKQNSKIDVHREMGAA 240  
QY 241 EKSTIIISTPEGSTSACKSILEIMKEKODIKFTEELPKILAHNNFVGRGLGEGRNK 300  
Db 241 EKSTIIISTPEGSTSACKSILEIMKEKODIKFTEELPKILAHNNFVGRGLGEGRNK 300  
QY 301 KIEODTDTKITISPLQDELTYNPERTIVKGNVETCAKAEELIMKIRISTENDIASNL 360  
Db 301 KIEODTDTKITISPLQDELTYNPERTIVKGNVETCAKAEELIMKIRISTENDIASNL 360



```

QY 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPPTPYQFQSETEVHOFIPALSVGAI 420
DB 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPPTPYQFQSETEVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMMVITTPPEAOKRAGRIYGIKKEENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMMVITTPPEAOKRAGRIYGIKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVELNOLNLSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVELNOLNLSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACOVAKRKIOELITVOYKHOQOKALQSGPPQSRK 579
DB 541 GHFYACOVAKRKIOELITVOYKHOQOKALQSGPPQSRK 579

```

## RESULT 8

```

US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

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Query Match 65.1%; Score 377; DB 10; Length 579;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MNKIYIGLSNAPSDLESIFKDAKIPVSGPPLVKTGYAFVDCPDSEWALKATLALSGK 60
DB 1 MNKIYIGLSNAPSDLESIFKDAKIPVSGPPLVKTGYAFVDCPDSEWALKATLALSGK 60
QY 61 ELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSETA 120
DB 61 ELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSETA 120
QY 121 VVNTYSSKDOARALDKLNGFOLENTLKVAIIPDEMAAQNPLQOPGRGRLGORGSS 180
DB 121 VVNTYSSKDOARALDKLNGFOLENTLKVAIIPDEMAAQNPLQOPGRGRLGORGSS 180
QY 181 ROGSPGVSOKPCDPLRLVLPOTFVGALIGKEGATIRNITKOTOSKIDVHRKKNAGAA 240
DB 181 ROGSPGVSOKPCDPLRLVLPOTFVGALIGKEGATIRNITKOTOSKIDVHRKKNAGAA 240
QY 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPKILAHNFVGRLLGKGRNKK 300
DB 241 EKSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPKILAHNFVGRLLGKGRNKK 300
QY 301 KIEQDTDKITISPLQELITLYNPERITVYKGNVETCAKAEELIMKIRRESYENDIASMNL 360
DB 301 KIEQDTDKITISPLQELITLYNPERITVYKGNVETCAKAEELIMKIRRESYENDIASMNL 360

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QY 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPPTPYQFQSETEVHOFIPALSVGAI 420
DB 361 QAHILPGLNMLNGLPPTSGMPPTSGPPSAMPPTPYQFQSETEVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMMVITTPPEAOKRAGRIYGIKKEENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVMMVITTPPEAOKRAGRIYGIKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVELNOLNLSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVELNOLNLSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACOVAKRKIOELITVOYKHOQOKALQSGPPQSRK 579
DB 541 GHFYACOVAKRKIOELITVOYKHOQOKALQSGPPQSRK 579

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## RESULT 9

```

US-09-850-716A-427
; Sequence 427, Application US/09850716A
; Patent No. US2002015139A1
; GENERAL INFORMATION:
; APPLICANT: Kaelos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reltzer, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-427

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Query Match 64.9%; Score 376; DB 10; Length 586;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 NKLIYIGLSNAPSDLESIFKDAKIPVSGPPLVKTGYAFVDCPDSEWALKATLALSGK 61
DB 2 NKLIYIGLSNAPSDLESIFKDAKIPVSGPPLVKTGYAFVDCPDSEWALKATLALSGK 61
QY 62 ELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSETA 121
DB 62 ELHGKPIEVESHVPRKQRIKRLQIRNIPHLQMEVLDLSLVQYGVESCEQVNTDSETA 121
QY 122 VVNTYSSKDOARALDKLNGFOLENTLKVAIIPDEMAAQNPLQOPGRGRLGORGSS 181
DB 122 VVNTYSSKDOARALDKLNGFOLENTLKVAIIPDEMAAQNPLQOPGRGRLGORGSS 181
QY 182 QGSPGVSOKPCDPLRLVLPOTFVGALIGKEGATIRNITKOTOSKIDVHRKKNAGAA 241
DB 182 QGSPGVSOKPCDPLRLVLPOTFVGALIGKEGATIRNITKOTOSKIDVHRKKNAGAA 241
QY 242 KSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPKILAHNFVGRLLGKGRNKK 301
DB 242 KSTIIISTPEGSTSAACKSILEIMHKEADIKFTEELPKILAHNFVGRLLGKGRNKK 301
QY 302 IEQDTDKITISPLQELITLYNPERITVYKGNVETCAKAEELIMKIRRESYENDIASMNL 361
DB 302 IEQDTDKITISPLQELITLYNPERITVYKGNVETCAKAEELIMKIRRESYENDIASMNL 361
QY 362 AHIILPGLNMLNGLPPTSGMPPTSGPPSAMPPTPYQFQSETEVHOFIPALSVGAI 421
DB 362 AHIILPGLNMLNGLPPTSGMPPTSGPPSAMPPTPYQFQSETEVHOFIPALSVGAI 421
QY 422 IKGOGHITKOLSRFAGASIKIAPAPADAKVMMVITTPPEAOKRAGRIYGIKKEENFV 481
DB 422 IKGOGHITKOLSRFAGASIKIAPAPADAKVMMVITTPPEAOKRAGRIYGIKKEENFV 481
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVELNOLNLSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVELNOLNLSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACOVAKRKIOELITVOYKHOQOKALQSGPPQSRK 579
DB 541 GHFYACOVAKRKIOELITVOYKHOQOKALQSGPPQSRK 579

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QY 482 FREEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVYVPRDQTPDENDOVVVKITG 541  
DB 489 FREEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVYVPRDQTPDENDOVVVKITG 548  
QY 542 HEVACOVAORRICEILTVOKHOQOKALOSGPPSRRK 579  
DB 549 HEVACOVAORRICEILTVOKHOQOKALOSGPPSRRK 586

## RESULT 10

US-09-897-778-427  
Sequence 427, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897.778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 427  
LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-427

## Query Match

Best Local Similarity 64.9%; Score 376; DB 10; Length 586;  
Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKLYTGNLSENAAPSDLESIFDKANIPVSGFVLKGTGYAFVDCPDSENAKALKAIEALSGKI 61  
DB 9 NKLYTGNLSENAAPSDLESIFDKANIPVSGFVLKGTGYAFVDCPDSENAKALKAIEALSGKI 68  
QY 67 ELHGKPIEVEHSVPRKQRIKRLQIRNIPHLQWELDSLVOYGAVESCEQVNTDSEYAV 121  
DB 69 ELHGKPIEVEHSVPRKQRIKRLQIRNIPHLQWELDSLVOYGAVESCEQVNTDSEYAV 128  
QY 122 VNVYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAOONPLOOPGRGRLGQRGSSR 181  
DB 129 VNVYSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAOONPLOOPGRGRLGQRGSSR 188  
QY 182 QGSPGSVSKORPCDLRLVLVPTQFVGAITGKEGATIRNITKOTOSKIDVRRKENAAGAE 241  
DB 189 QGSPGSVSKORPCDLRLVLVPTQFVGAITGKEGATIRNITKOTOSKIDVRRKENAAGAE 248  
QY 242 KSTITLSTPREGTSAAKSLILEMHEKADIKETFEELPLKLIANNFVRLIGKGRMLK 301  
DB 249 KSTITLSTPREGTSAAKSLILEMHEKADIKETFEELPLKLIANNFVRLIGKGRMLK 308  
QY 302 IEODTDRKITISPLQELTYNPERTITVKGVETCAKAEELMKIRSYENDJASNLQ 361  
DB 309 IEODTDRKITISPLQELTYNPERTITVKGVETCAKAEELMKIRSYENDJASNLQ 368  
QY 362 AHLIPGILNALALGIPPTSGMPPTSGPSAMTPPYPOFQOSTETVHOFIPALSGAIL 421  
DB 369 AHLIPGILNALALGIPPTSGMPPTSGPSAMTPPYPOFQOSTETVHOFIPALSGAIL 428  
QY 422 GKOGOHKOLSRFAGASIKIAPAEAPDAKVAVYINGPPEAOPFKAGRIYGIKEENFVS 481  
DB 429 GKOGOHKOLSRFAGASIKIAPAEAPDAKVAVYINGPPEAOPFKAGRIYGIKEENFVS 488

QY 482 FREEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVYVPRDQTPDENDOVVVKITG 541  
DB 489 FREEVKLEAHIRVPSFAAGRVIGKGTVNELONLSSAEVYVPRDQTPDENDOVVVKITG 548  
QY 542 HEVACOVAORRICEILTVOKHOQOKALOSGPPSRRK 579  
DB 549 HEVACOVAORRICEILTVOKHOQOKALOSGPPSRRK 586

## RESULT 11

US-09-864-761-48606  
Sequence 48606, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864.761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 48606  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC021876.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8  
OTHER INFORMATION: SWISSPROT HIT: 007244, EVALU 6.10e-01  
OTHER INFORMATION: EST\_HUMAN HIT: BE545535.1, EVALU 2.00e-09  
US-09-864-761-48606

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Query Match 16.1%; Score 93; DB 10; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.2e-82;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 135 ALDRKNGFQLENTFLKAVIPEMAAQNPLQOPGRKGLGGRGSSRGSSPSVSKORFC 194
Db 1 ALDRKNGFQLENTFLKAVIPEMAAQNPLQOPGRKGLGGRGSSRGSSPSVSKORFC 60

Oy 195 DLPLRLVPTQFVGAIIKREGATININIKOTOS 227
Db 61 DLPLRLVPTQFVGAIIKREGATININIKOTOS 93

RESULT 12
US-09-873-637-24
; Sequence 24, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873.637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-637-24

Query Match 8.3%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.4e-39;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 492 IRVPSFAGRYIIGKGTIVNELQNLSSAEVVPVRDQTPDENDQVVKI 539
Db 1 IRVPSFAGRYIIGKGTIVNELQNLSSAEVVPVRDQTPDENDQVVKI 48

RESULT 13
US-09-873-637-23
; Sequence 23, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873.637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-637-23

Query Match 8.1%; Score 47; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 6.7e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 410 QFIPALSGAIIIGKGGHIIKQLSRFAGSIRKIPAEAPDAKVRMYII 456
Db 1 QFIPALSGAIIIGKGGHIIKQLSRFAGSIRKIPAEAPDAKVRMYII 47

RESULT 14
US-09-864-761-45987
; Sequence 45987, Application US/09864761
; Patent No. US20020048763A1

; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864.761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180.312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207.456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632.366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236.359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234.687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608.408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774.203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45987
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021876.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: P78004, EVALU 2.80e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA427803.1, EVALU 9.00e-19
US-09-864-761-45987

Query Match 7.8%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.5e-36;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 315 LOELTYNPERITIVKGNVETCAKAEELMKIRSYENDIASMN 359
Db 1 LOELTYNPERITIVKGNVETCAKAEELMKIRSYENDIASMN 45

RESULT 15
US-09-873-637-22
; Sequence 22, Application US/09873637
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Thu Apr 17 07:55:17 2003

us-09-897-778-176.Oligo.rapb

Page 8

Patent No. US20020061543A1  
: GENERAL INFORMATION:  
: APPLICANT: Ross, Jeffrey  
: TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
: TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE  
: FILE REFERENCE: 960296.95131  
: CURRENT APPLICATION NUMBER: US/09/873,637  
: CURRENT FILING DATE: 2001-06-04  
: NUMBER OF SEQ ID NOS: 46  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 22  
: LENGTH: 49  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-873-637-22

Query Match 7.3%; Score 42; DB 10; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 288 VGRLLGEGGRNLKITEODTDRKITSPLQELTYNPERITV 329  
|||  
Db 8 VGRLLGEGGRNLKITEODTDRKITSPLQELTYNPERITV 49

Search completed: April 16, 2003, 16:48:41  
Job time: 67.3517 secs

GenCore version 5.1.4\_p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:34:47 ; Search time 392.655 Seconds  
(without alignments)  
950.708 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579  
Sequence: 1 MNKLYIGNLSENAAPSDLES.....VKHQOQKALQSGPPQSRK 579

Scoring table:  
Gapop 60.0, Gapext 60.0

Searched: 4569144 segs, 644733110 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/paa/US06.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US081.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US082.COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US083.COMB.pep.\*
- 8: /cgn2\_6/ptodata/1/paa/US084.COMB.pep.\*
- 9: /cgn2\_6/ptodata/1/paa/US085.COMB.pep.\*
- 10: /cgn2\_6/ptodata/1/paa/US086.COMB.pep.\*
- 11: /cgn2\_6/ptodata/1/paa/US087.COMB.pep.\*
- 12: /cgn2\_6/ptodata/1/paa/US088.COMB.pep.\*
- 13: /cgn2\_6/ptodata/1/paa/US090.COMB.pep.\*
- 14: /cgn2\_6/ptodata/1/paa/US091.COMB.pep.\*
- 15: /cgn2\_6/ptodata/1/paa/US092.COMB.pep.\*
- 16: /cgn2\_6/ptodata/1/paa/US093.COMB.pep.\*
- 17: /cgn2\_6/ptodata/1/paa/US094.COMB.pep.\*
- 18: /cgn2\_6/ptodata/1/paa/US095.COMB.pep.\*
- 19: /cgn2\_6/ptodata/1/paa/US096.COMB.pep.\*
- 20: /cgn2\_6/ptodata/1/paa/US097.COMB.pep.\*
- 21: /cgn2\_6/ptodata/1/paa/US098.COMB.pep.\*
- 22: /cgn2\_6/ptodata/1/paa/US099.COMB.pep.\*
- 23: /cgn2\_6/ptodata/1/paa/US100.COMB.pep.\*
- 24: /cgn2\_6/ptodata/1/paa/US101.COMB.pep.\*
- 25: /cgn2\_6/ptodata/1/paa/US102.COMB.pep.\*
- 26: /cgn2\_6/ptodata/1/paa/US103.COMB.pep.\*
- 27: /cgn2\_6/ptodata/1/paa/US60.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	579	1	PCT-US01-47576-176
2	579	100.0	579	18	US-09-466-396A-176
3	579	100.0	579	18	US-09-476-496A-176
4	579	100.0	579	18	US-09-480-884A-176
5	579	100.0	579	19	US-09-510-376A-176
6	579	100.0	579	19	US-09-542-615A-176

7	579	100.0	579	20	US-09-606-421A-176	Sequence 176, App
8	579	100.0	579	20	US-09-606-421B-176	Sequence 176, App
9	579	100.0	579	20	US-09-630-940A-176	Sequence 176, App
10	579	100.0	579	20	US-09-630-940B-176	Sequence 176, App
11	579	100.0	579	20	US-09-662-786-176	Sequence 176, App
12	579	100.0	579	20	US-09-685-696-176	Sequence 176, App
13	579	100.0	579	21	US-09-735-705-176	Sequence 176, App
14	579	100.0	579	21	US-09-791-537-49019	Sequence 49019, A
15	579	100.0	579	22	US-09-850-716-176	Sequence 176, App
16	579	100.0	579	22	US-09-850-716A-176	Sequence 176, App
17	579	100.0	579	22	US-09-897-778-176	Sequence 176, App
18	579	100.0	579	24	US-10-007-700-176	Sequence 176, App
19	579	100.0	579	25	US-10-117-982-176	Sequence 176, App
20	478	82.6	579	25	US-09-791-537-86130	Sequence 86130, A
21	398	68.7	579	25	US-10-117-982-484	Sequence 484, App
22	377	65.1	579	1	PCT-US01-47576-348	Sequence 348, App
23	377	65.1	579	1	PCT-US01-47576-446	Sequence 446, App
24	377	65.1	579	1	PCT-US01-47576-449	Sequence 449, App
25	377	65.1	579	19	US-09-542-615A-348	Sequence 348, App
26	377	65.1	579	20	US-09-606-421A-348	Sequence 348, App
27	377	65.1	579	20	US-09-606-421B-348	Sequence 348, App
28	377	65.1	579	20	US-09-630-940A-348	Sequence 348, App
29	377	65.1	579	20	US-09-630-940B-348	Sequence 348, App
30	377	65.1	579	20	US-09-662-786-348	Sequence 348, App
31	377	65.1	579	20	US-09-685-696-348	Sequence 348, App
32	377	65.1	579	21	US-09-735-705-348	Sequence 348, App
33	377	65.1	579	22	US-09-850-716-348	Sequence 348, App
34	377	65.1	579	22	US-09-850-716A-348	Sequence 348, App
35	377	65.1	579	22	US-09-897-778-348	Sequence 348, App
36	377	65.1	579	22	US-09-897-778-446	Sequence 446, App
37	377	65.1	579	22	US-09-897-778-449	Sequence 449, App
38	377	65.1	579	24	US-10-007-700-348	Sequence 348, App
39	377	65.1	579	24	US-10-007-700-446	Sequence 446, App
40	377	65.1	579	24	US-10-007-700-449	Sequence 449, App
41	377	65.1	579	25	US-10-117-982-348	Sequence 348, App
42	377	65.1	579	25	US-10-117-982-446	Sequence 446, App
43	377	65.1	579	25	US-10-117-982-449	Sequence 449, App
44	377	65.1	579	25	US-10-117-982-480	Sequence 480, App
45	376	64.9	586	1	PCT-US01-47576-427	Sequence 427, App

#### ALIGNMENTS

RESULT 1  
PCT-US01-47576-176  
; Sequence 176, Application PC/TUS0147576  
; GENERAL INFORMATION:  
; APPLICANT: Corixa Corporation  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; APPLICANT: Reiter, Marc W.  
; APPLICANT: Durham, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvik, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Peckman, David W.  
; APPLICANT: Cai, Feng  
; APPLICANT: Fay, Teresa M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.45503PC  
; CURRENT APPLICATION NUMBER: PCT/US01/47576  
; CURRENT FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0

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Page 2

SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US01-47576-176

Query Match 100.0%; Score 579; DB 1; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60
DB 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60
OY 61 IELHGKPIEIVHSVKKRRIKQIRNIPPHLOMEVLSLVOYGVESECVNTDSETA 120
DB 61 IELHGKPIEIVHSVKKRRIKQIRNIPPHLOMEVLSLVOYGVESECVNTDSETA 120
OY 121 VVAVYSSKQARQALDKLNGFLENFTLVKAVIPDEMAAOQNPLOQPRGRGLGGRSS 180
DB 121 VVAVYSSKQARQALDKLNGFLENFTLVKAVIPDEMAAOQNPLOQPRGRGLGGRSS 180
OY 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTQSKIDVHKRENAGAA 240
DB 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTQSKIDVHKRENAGAA 240
OY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRLLICEGRNLK 300
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRLLICEGRNLK 300
OY 301 KIEQDDTKITITSPLOELITLVNPERTTVKGNVETCAKAEELIMKKIRESYENDIASMNL 360
DB 301 KIEQDDTKITITSPLOELITLVNPERTTVKGNVETCAKAEELIMKKIRESYENDIASMNL 360
OY 361 QAHILPGLNLNLGLFPPTSQMPPTSGPPSAMPPTPYQFQSEETETVHOFIPALSVGAI 420
DB 361 QAHILPGLNLNLGLFPPTSQMPPTSGPPSAMPPTPYQFQSEETETVHOFIPALSVGAI 420
OY 421 IGKQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPPEAOFRKAGRIYGIKEENFV 480
DB 421 IGKQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPPEAOFRKAGRIYGIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPENDQVYVKKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPENDQVYVKKIT 540
OY 541 GHFYACQVAKRKIOEILTVQVKKHQQOKALQSGPQSRK 579
DB 541 GHFYACQVAKRKIOEILTVQVKKHQQOKALQSGPQSRK 579
```

RESULT 2  
US-09-466-396A-176  
Sequence 176, Application US/09466396A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.455C4  
CURRENT APPLICATION NUMBER: US/09/466.396A  
CURRENT FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-466-396A-176

Query Match 100.0%; Score 579; DB 18; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60
DB 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60
OY 61 IELHGKPIEIVHSVKKRRIKQIRNIPPHLOMEVLSLVOYGVESECVNTDSETA 120
DB 61 IELHGKPIEIVHSVKKRRIKQIRNIPPHLOMEVLSLVOYGVESECVNTDSETA 120
OY 121 VVAVYSSKQARQALDKLNGFLENFTLVKAVIPDEMAAOQNPLOQPRGRGLGGRSS 180
DB 121 VVAVYSSKQARQALDKLNGFLENFTLVKAVIPDEMAAOQNPLOQPRGRGLGGRSS 180
OY 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTQSKIDVHKRENAGAA 240
DB 181 RQSPGSVSKQPCDLPRLVPTQFVGALIGEGATIRNITKOTQSKIDVHKRENAGAA 240
OY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRLLICEGRNLK 300
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKILAHNNFVGRLLICEGRNLK 300
OY 301 KIEQDDTKITITSPLOELITLVNPERTTVKGNVETCAKAEELIMKKIRESYENDIASMNL 360
DB 301 KIEQDDTKITITSPLOELITLVNPERTTVKGNVETCAKAEELIMKKIRESYENDIASMNL 360
OY 361 QAHILPGLNLNLGLFPPTSQMPPTSGPPSAMPPTPYQFQSEETETVHOFIPALSVGAI 420
DB 361 QAHILPGLNLNLGLFPPTSQMPPTSGPPSAMPPTPYQFQSEETETVHOFIPALSVGAI 420
OY 421 IGKQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPPEAOFRKAGRIYGIKEENFV 480
DB 421 IGKQGHIKOLSRFAGASIKIAPAEADAKVRNVIITGPPEAOFRKAGRIYGIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPENDQVYVKKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGGKTVNELQNLSSAEVYVPRDQTPENDQVYVKKIT 540
OY 541 GHFYACQVAKRKIOEILTVQVKKHQQOKALQSGPQSRK 579
DB 541 GHFYACQVAKRKIOEILTVQVKKHQQOKALQSGPQSRK 579
```

RESULT 3  
US-09-476-496A-176  
Sequence 176, Application US/09476496A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF  
FILE REFERENCE: 210121.455C5  
CURRENT APPLICATION NUMBER: US/09/476.496A  
CURRENT FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 254  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-476-496A-176

Query Match 100.0%; Score 579; DB 18; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60
DB 1 MNKLYIGNSENAPSDLESIFKDAKIPVSGPFLVTCGAFVDCPDDESMALKAIEALSCK 60
OY 61 IELHGKPIEIVHSVKKRRIKQIRNIPPHLOMEVLSLVOYGVESECVNTDSETA 120
DB 61 IELHGKPIEIVHSVKKRRIKQIRNIPPHLOMEVLSLVOYGVESECVNTDSETA 120
```

```

Qy 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAATIPDEMAAOQNPLOQPRGRGLGGRSS 180
    |||||||
Db 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAATIPDEMAAOQNPLOQPRGRGLGGRSS 180
Qy 181 RGSFGSVSKOKPCDPLRLVPTQFVGAIIIGKEGATIRNTKOTQSKIDVHRKENAGAA 240
    |||||||
Db 181 RGSFGSVSKOKPCDPLRLVPTQFVGAIIIGKEGATIRNTKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTIILSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNILK 300
    |||||||
Db 241 EKSTIILSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNILK 300
Qy 301 KIEDOTDKITITSPLOELTYNPERTIVKGNVETCAKAEELMKKIRESEYENDIASMNL 360
    |||||||
Db 301 KIEDOTDKITITSPLOELTYNPERTIVKGNVETCAKAEELMKKIRESEYENDIASMNL 360
Qy 361 QAHILPGLNMLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
    |||||||
Db 361 QAHILPGLNMLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
Qy 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAGRIYGIKEENFV 480
    |||||||
Db 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAGRIYGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTKVNELOMLSSAEVVPBDQTPDENQVVKIT 540
    |||||||
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTKVNELOMLSSAEVVPBDQTPDENQVVKIT 540
Qy 541 GHFYACOVAORKIOELITVOVKHOQKALOSGPPQSRK 579
    |||||||
Db 541 GHFYACOVAORKIOELITVOVKHOQKALOSGPPQSRK 579

```

## RESULT 4

```

US-09-480-884A-176
: Sequence 176, Application US/09480884A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C6
: CURRENT APPLICATION NUMBER: US/09/480.884A
: CURRENT FILING DATE: 2001-08-27
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-480-884A-176

```

```

Query Match          100.0%; Score 579; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
    |||||||
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
Qy 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLVOYGVVESCQVNTDSETA 120
    |||||||
Db 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLVOYGVVESCQVNTDSETA 120
Qy 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAATIPDEMAAOQNPLOQPRGRGLGGRSS 180
    |||||||
Db 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAATIPDEMAAOQNPLOQPRGRGLGGRSS 180
Qy 181 RGSFGSVSKOKPCDPLRLVPTQFVGAIIIGKEGATIRNTKOTQSKIDVHRKENAGAA 240
    |||||||

```

```

Db 181 RGSFGSVSKOKPCDPLRLVPTQFVGAIIIGKEGATIRNTKOTQSKIDVHRKENAGAA 240
    |||||||
Qy 241 EKSTIILSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNILK 300
    |||||||
Db 241 EKSTIILSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNILK 300
Qy 301 KIEDOTDKITITSPLOELTYNPERTIVKGNVETCAKAEELMKKIRESEYENDIASMNL 360
    |||||||
Db 301 KIEDOTDKITITSPLOELTYNPERTIVKGNVETCAKAEELMKKIRESEYENDIASMNL 360
Qy 361 QAHILPGLNMLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
    |||||||
Db 361 QAHILPGLNMLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFPALSVGAI 420
Qy 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAGRIYGIKEENFV 480
    |||||||
Db 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAOFKAGRIYGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTKVNELOMLSSAEVVPBDQTPDENQVVKIT 540
    |||||||
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTKVNELOMLSSAEVVPBDQTPDENQVVKIT 540
Qy 541 GHFYACOVAORKIOELITVOVKHOQKALOSGPPQSRK 579
    |||||||
Db 541 GHFYACOVAORKIOELITVOVKHOQKALOSGPPQSRK 579

```

## RESULT 5

```

US-09-510-376A-176
: Sequence 176, Application US/09510376A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C7
: CURRENT APPLICATION NUMBER: US/09/510.376A
: CURRENT FILING DATE: 2001-08-21
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-510-376A-176

```

```

Query Match          100.0%; Score 579; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
    |||||||
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
Qy 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLVOYGVVESCQVNTDSETA 120
    |||||||
Db 61 IELHGKPIEVEHSVPRKORIRKLOIRNIPHLQWEVLDLSLVOYGVVESCQVNTDSETA 120
Qy 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAATIPDEMAAOQNPLOQPRGRGLGGRSS 180
    |||||||
Db 121 VVNVYSSKDOARQALDKLNGFOLNFTLKVAATIPDEMAAOQNPLOQPRGRGLGGRSS 180
Qy 181 RGSFGSVSKOKPCDPLRLVPTQFVGAIIIGKEGATIRNTKOTQSKIDVHRKENAGAA 240
    |||||||
Db 181 RGSFGSVSKOKPCDPLRLVPTQFVGAIIIGKEGATIRNTKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTIILSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNILK 300
    |||||||
Db 241 EKSTIILSTPEGTSAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGEGRNILK 300

```

```

QY 301 KIEODTPKRTIISPLQELTYNPERTITVKNVETCAKAEELMKKIRESEYENDIASMNL 360
DB 301 KIEODTPKRTIISPLQELTYNPERTITVKNVETCAKAEELMKKIRESEYENDIASMNL 360
QY 361 QAHLLPGLNMLALGLPPTSGMPPTSGPSPAMTPPYPOFEOSETETVHOEIPALSVGAI 420
DB 361 QAHLLPGLNMLALGLPPTSGMPPTSGPSPAMTPPYPOFEOSETETVHOEIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVRWYITIGPPEAOFKAOGRIYGIKEENFY 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVRWYITIGPPEAOFKAOGRIYGIKEENFY 480
QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVELQNLSSAEVVVPRDQTPDENDDVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVELQNLSSAEVVVPRDQTPDENDDVVVKIT 540
QY 541 GHFYACVAAORKIOEILITOVKOHQOKALOSGPQSRK 579
DB 541 GHFYACVAAORKIOEILITOVKOHQOKALOSGPQSRK 579

RESULT 6
US-09-542-615A-176
: Sequence 176, Application US/09542615A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaltanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Skelky, Yasir A.W.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C8
: CURRENT APPLICATION NUMBER: US/09/542.615A
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-542-615A-176

```

```

Query Match      100.0%; Score 579; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSNNAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
DB 1 MNKLYIGNLSNNAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
QY 61 IELHGKPIEVEHVSVPKROIRIKLOIRNIPPHLOMEVLDLSLVQGVVSCQVNTDSETA 120
DB 61 IELHGKPIEVEHVSVPKROIRIKLOIRNIPPHLOMEVLDLSLVQGVVSCQVNTDSETA 120
QY 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGCGSS 180
DB 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGCGSS 180
QY 181 ROGSPGSVSKOKPCDPLRLILVPTQFVGAILGEGATIRNITKQOSKIDVHREKNGAA 240
DB 181 ROGSPGSVSKOKPCDPLRLILVPTQFVGAILGEGATIRNITKQOSKIDVHREKNGAA 240
QY 241 EKSTIISTPEGSTSAACKSILEIMHKEADIKTEETIPLKLAHNNFGRIGEGENLK 300
DB 241 EKSTIISTPEGSTSAACKSILEIMHKEADIKTEETIPLKLAHNNFGRIGEGENLK 300
QY 301 KIEODTPKRTIISPLQELTYNPERTITVKNVETCAKAEELMKKIRESEYENDIASMNL 360
DB 301 KIEODTPKRTIISPLQELTYNPERTITVKNVETCAKAEELMKKIRESEYENDIASMNL 360

```

```

QY 361 QAHLLPGLNMLALGLPPTSGMPPTSGPSPAMTPPYPOFEOSETETVHOEIPALSVGAI 420
DB 361 QAHLLPGLNMLALGLPPTSGMPPTSGPSPAMTPPYPOFEOSETETVHOEIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVRWYITIGPPEAOFKAOGRIYGIKEENFY 480
DB 421 IKGOGHITKOLSRFAGASIKIAPAPADAKVRWYITIGPPEAOFKAOGRIYGIKEENFY 480
QY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVELQNLSSAEVVVPRDQTPDENDDVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVELQNLSSAEVVVPRDQTPDENDDVVVKIT 540
QY 541 GHFYACVAAORKIOEILITOVKOHQOKALOSGPQSRK 579
DB 541 GHFYACVAAORKIOEILITOVKOHQOKALOSGPQSRK 579

```

```

RESULT 7
US-09-606-421A-176
: Sequence 176, Application US/09606421A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaltanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C9
: CURRENT APPLICATION NUMBER: US/09/606.421A
: NUMBER OF SEQ ID NOS: 354
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-606-421A-176

```

```

Query Match      100.0%; Score 579; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSNNAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
DB 1 MNKLYIGNLSNNAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSCK 60
QY 61 IELHGKPIEVEHVSVPKROIRIKLOIRNIPPHLOMEVLDLSLVQGVVSCQVNTDSETA 120
DB 61 IELHGKPIEVEHVSVPKROIRIKLOIRNIPPHLOMEVLDLSLVQGVVSCQVNTDSETA 120
QY 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGCGSS 180
DB 121 VVNTYSSKQDARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGCGSS 180
QY 181 ROGSPGSVSKOKPCDPLRLILVPTQFVGAILGEGATIRNITKQOSKIDVHREKNGAA 240
DB 181 ROGSPGSVSKOKPCDPLRLILVPTQFVGAILGEGATIRNITKQOSKIDVHREKNGAA 240
QY 241 EKSTIISTPEGSTSAACKSILEIMHKEADIKTEETIPLKLAHNNFGRIGEGENLK 300
DB 241 EKSTIISTPEGSTSAACKSILEIMHKEADIKTEETIPLKLAHNNFGRIGEGENLK 300
QY 301 KIEODTPKRTIISPLQELTYNPERTITVKNVETCAKAEELMKKIRESEYENDIASMNL 360
DB 301 KIEODTPKRTIISPLQELTYNPERTITVKNVETCAKAEELMKKIRESEYENDIASMNL 360
QY 361 QAHLLPGLNMLALGLPPTSGMPPTSGPSPAMTPPYPOFEOSETETVHOEIPALSVGAI 420
DB 361 QAHLLPGLNMLALGLPPTSGMPPTSGPSPAMTPPYPOFEOSETETVHOEIPALSVGAI 420

```



Db 361 QAHILPGLNALGLFPPTSGMPPTSGPPSAMPPTPYQFQSETEYVHOFIPALSVGAI 420  
Qy 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITIGPEAOFKAGRIYGIKEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITIGPEAOFKAGRIYGIKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGRVIGKGGTYVNELONSAEVVPROTDENDQVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGGTYVNELONSAEVVPROTDENDQVVKIT 540  
Qy 541 GHFYACQVAORRTOELITVOKHOQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORRTOELITVOKHOQOKALQSGPPQSRK 579

RESULT 8  
US-09-606-421B-176  
; Sequence 176, Application US/09606421B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606,421B  
; CURRENT FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-606-421B-176

Query Match 100.0%; Score 579; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Qy 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDLSLVQYGVESCEQVNTDSEFA 120  
Db 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDLSLVQYGVESCEQVNTDSEFA 120  
Qy 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPLOQPRGRRLGGRSS 180  
Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPLOQPRGRRLGGRSS 180  
Qy 181 ROGSPGSVSKQKPCDPLRLVPTQFVGAITGEGATIRNITKOTQSKIDVHKRENAAGAA 240  
Db 181 ROGSPGSVSKQKPCDPLRLVPTQFVGAITGEGATIRNITKOTQSKIDVHKRENAAGAA 240  
Qy 241 EKSTILSTPEGSTAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRLLGEGRNK 300  
Db 241 EKSTILSTPEGSTAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRLLGEGRNK 300  
Qy 301 KIEODTDTKITISPLQELTYNPERTTVKGNVETCAKAEELIMKIRIESTENDIASMNL 360  
Db 301 KIEODTDTKITISPLQELTYNPERTTVKGNVETCAKAEELIMKIRIESTENDIASMNL 360  
Qy 361 QAHILPGLNALGLFPPTSGMPPTSGPPSAMPPTPYQFQSETEYVHOFIPALSVGAI 420  
Db 361 QAHILPGLNALGLFPPTSGMPPTSGPPSAMPPTPYQFQSETEYVHOFIPALSVGAI 420

Qy 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITIGPEAOFKAGRIYGIKEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRWVITIGPEAOFKAGRIYGIKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGRVIGKGGTYVNELONSAEVVPROTDENDQVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGGTYVNELONSAEVVPROTDENDQVVKIT 540  
Qy 541 GHFYACQVAORRTOELITVOKHOQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORRTOELITVOKHOQOKALQSGPPQSRK 579

RESULT 9  
US-09-630-940A-176  
; Sequence 176, Application US/09630940A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skelky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455G10  
; CURRENT APPLICATION NUMBER: US/09/630,940A  
; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-630-940A-176

Query Match 100.0%; Score 579; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSGK 60  
Qy 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDLSLVQYGVESCEQVNTDSEFA 120  
Db 61 IELHGKPIEVEHSVPRKRIKRLQIRNIPHLQWEVLDLSLVQYGVESCEQVNTDSEFA 120  
Qy 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPLOQPRGRRLGGRSS 180  
Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNLPLOQPRGRRLGGRSS 180  
Qy 181 ROGSPGSVSKQKPCDPLRLVPTQFVGAITGEGATIRNITKOTQSKIDVHKRENAAGAA 240  
Db 181 ROGSPGSVSKQKPCDPLRLVPTQFVGAITGEGATIRNITKOTQSKIDVHKRENAAGAA 240  
Qy 241 EKSTILSTPEGSTAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRLLGEGRNK 300  
Db 241 EKSTILSTPEGSTAACKSILEIMHKEADIKFTEIPLKILAHNNFVGRLLGEGRNK 300  
Qy 301 KIEODTDTKITISPLQELTYNPERTTVKGNVETCAKAEELIMKIRIESTENDIASMNL 360  
Db 301 KIEODTDTKITISPLQELTYNPERTTVKGNVETCAKAEELIMKIRIESTENDIASMNL 360  
Qy 361 QAHILPGLNALGLFPPTSGMPPTSGPPSAMPPTPYQFQSETEYVHOFIPALSVGAI 420  
Db 361 QAHILPGLNALGLFPPTSGMPPTSGPPSAMPPTPYQFQSETEYVHOFIPALSVGAI 420

Thu Apr 17 07:55:17 2003

us-09-897-778-176.Oligo.rapm

Page 6

Qy	421	IKKQSGHFKOLSPKASAKITLAPADPAVVRVITITPPKQKAGRIYKITEENV	480
Db	421	IKKQSGHFKOLSPKASAKITLAPADPAVVRVITITPPKQKAGRIYKITEENV	480
Qy	481	SPKEEVKLEAHINVPFAGRIYKIGKRYNELNLSAEVYVVRROOTPDENDQYVAKIT	540
Db	481	SPKEEVKLEAHINVPFAGRIYKIGKRYNELNLSAEVYVVRROOTPDENDQYVAKIT	540
Qy	541	GHEFYACQYAKQKIDELLIVYKQHQQAKALSGPPOSRRK	579
Db	541	GHEFYACQYAKQKIDELLIVYKQHQQAKALSGPPOSRRK	579

```

RESULT 10
US-09-630-940B-176
Sequence 176. Application US/09630940B
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Lidan
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Panger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Jasir A.W
APPLICANT: Hendetson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSTIS OF LUNG CANCER
FILE REFERENCE: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630.940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-630-940B-176

```

Query Match	Similarity	100.0%	Score 579	DB 20	Length 579
Best Local Similarity	100.0%	Pred. No. 0			
Matches 579	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	MNLYIGNLSEMAAPSDLESIFDQAKIPYSGFPLKGTGYAFVDCPDSESNALKAIEALS	SGK	60	
Db	1	MNLYIGNLSEMAAPSDLESIFDQAKIPYSGFPLKGTGYAFVDCPDSESNALKAIEALS	SGK	60	
QY	61	IELHGKPIEVESHVPRKORIRKLOIRNIPPIHLOWEVLDSLLVYGVVESCQEVNDSE	ETA	120	
Db	61	IELHGKPIEVESHVPRKORIRKLOIRNIPPIHLOWEVLDSLLVYGVVESCQEVNDSE	ETA	120	
QY	121	VVWVYSSKCDARALDKLNGFLENTLKAAVYIPDMAQOONPLOORPGRGIGOGSS	180		
Db	121	VVWVYSSKCDARALDKLNGFLENTLKAAVYIPDMAQOONPLOORPGRGIGOGSS	180		
QY	181	ROGSGVSKKPCDDPLRLVYTOGVGAILGKGATIRNITRYKOTOSKIDVHKREMGAA	240		
Db	181	ROGSGVSKKPCDDPLRLVYTOGVGAILGKGATIRNITRYKOTOSKIDVHKREMGAA	240		
QY	241	EKSTIILSTPEGTSIAACKSTLEIMKREADIKFEELIRPKILAHNNFVGRILGKEGRN	LK	300	
Db	241	EKSTIILSTPEGTSIAACKSTLEIMKREADIKFEELIRPKILAHNNFVGRILGKEGRN	LK	300	
QY	301	KLEODTDKTIISPLDELTYNPERTIVKGNVETCAKKEEIMKIKESYEENDIASMN	L	360	
Db	301	KLEODTDKTIISPLDELTYNPERTIVKGNVETCAKKEEIMKIKESYEENDIASMN	L	360	
QY	361	QAHLLPGINLALGIRPPTSGMPRTSGPSBAMPPYPOFODESEIETYHOETPALSYGAT	420		
Db	361	QAHLLPGINLALGIRPPTSGMPRTSGPSBAMPPYPOFODESEIETYHOETPALSYGAT	420		

QY	421	IGKGGHIIKQLSFEASASIKIPAPAPAKRWIITGPPEDAFKNOGRTGKIKENFV	480
Db	421	IGKGGHIIKQLSFEASASIKIPAPAPAKRWIITGPPEDAFKNOGRTGKIKENFV	480
QY	481	SPKEVYVLEHIVPSPFAAGRVIGKGGTVELNLSSAEVVPDPDPDNDVVYKIT	540
Db	481	SPKEVYVLEHIVPSPFAAGRVIGKGGTVELNLSSAEVVPDPDPDNDVVYKIT	540
QY	541	GHTFACQVAQRKIQELILVYKHOQDQALDSGPPQSRK	579
Db	541	GHTFACQVAQRKIQELILVYKHOQDQALDSGPPQSRK	579

```

RESULT 11
? Sequence 176-786-176
? GENERAL INFORMATION:
? APPLICANT: Wang, Tongtong
? APPLICANT: Pan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aijun
? APPLICANT: Skelky, Isaac A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: Menelli, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.455C12
? CURRENT APPLICATION NUMBER: US/09/662.786
? CURRENT FILING DATE: 2000-09-15
? NUMBER OF SEQ ID NOS: 381
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 176
? LENGTH: 579
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-662-786-176

```

Query Match	Similarity	100.0%	Score	579:	DB	Length	579:
Best Local	Similarity	100.0%	Pred. NO. 0:				
Matches	579:	Conservative	0:	Mismatches	0:	Indels	0:
							Gaps
							0:
QY	1	MKKLYIGLSNNAAPSDLESIEFKDAKIPVSCSPPLVKTGVAFVDCDESMALKAIEALSGK	60				
Db	1	MKKLYIGLSNNAAPSDLESIEFKDAKIPVSCSPPLVKTGVAFVDCDESMALKAIEALSGK	60				
QY	61	IELHGKPIEVEHVSYPKKRORIRKIQIRNIPRLQMEVLDLSLVOYGAVESCEQVNTDETA	120				
Db	61	IELHGKPIEVEHVSYPKKRORIRKIQIRNIPRLQMEVLDLSLVOYGAVESCEQVNTDETA	120				
QY	121	VVNVTVSSKQDARALDKLNGFOLENFTLKVAAYIPDEMAAQNPLQDQGRGRGIGQSSS	180				
Db	121	VVNVTVSSKQDARALDKLNGFOLENFTLKVAAYIPDEMAAQNPLQDQGRGRGIGQSSS	180				
QY	181	RGSGSGSYSKQKRDPLRLPLVLPQFVAILGKGKGAATIRNTKQTSKIDVHRKENGAA	240				
Db	181	RGSGSGSYSKQKRDPLRLPLVLPQFVAILGKGKGAATIRNTKQTSKIDVHRKENGAA	240				
QY	241	EKSITILISFDEGTSAAKSGSILETMHKEADIKFEEELPKLILAHNNFAGRLIGKEGRNKL	300				
Db	241	EKSITILISFDEGTSAAKSGSILETMHKEADIKFEEELPKLILAHNNFAGRLIGKEGRNKL	300				
QY	301	KLEODPTKTLTIPRLDELFLVPEPTIVKGVETCAKKEEIMMKIKESYEENDIASMNL	360				
Db	301	KLEODPTKTLTIPRLDELFLVPEPTIVKGVETCAKKEEIMMKIKESYEENDIASMNL	360				
QY	361	GAHILPGANLNALGRLPPTSGMPPTSGSPSANTPRYPQFQESSEFETYHQPITALSYGAI	420				
Db	361	GAHILPGANLNALGRLPPTSGMPPTSGSPSANTPRYPQFQESSEFETYHQPITALSYGAI	420				

OY 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVWVITITGPEAOFKAGRIYKIKEENV 480  
| | | | |  
Db 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVWVITITGPEAOFKAGRIYKIKEENV 480  
OY 481 SPKEEVLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPVRDÖTPENDÖVVVKIT 540  
| | | | |  
Db 481 SPKEEVLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPVRDÖTPENDÖVVVKIT 540  
OY 541 GHFYACVQAORRKIDIELITQYKOHQOKALOSGPPQSRK 579  
| | | | |  
Db 541 GHFYACVQAORRKIDIELITQYKOHQOKALOSGPPQSRK 579

## RESULT 12

US-09-685-696-176  
; Sequence 176, Application us/09685696  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaltanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C13  
; CURRENT APPLICATION NUMBER: us/09/685.696  
; CURRENT FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-685-696-176

Query Match 100.0%; Score 579; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
| | | | |  
Db 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
OY 61 IELHGKPIEVHSVPKROIRIKLOIRNIPHLÖMEVLDLSLVOYGVESECOYNTDSETA 120  
| | | | |  
Db 61 IELHGKPIEVHSVPKROIRIKLOIRNIPHLÖMEVLDLSLVOYGVESECOYNTDSETA 120  
OY 121 VVNVVYSSKDOARÖALDLKNGFÖLENTFLKVAIYPDEMAAQÖNPLÖQPRGRGIGÖRGSS 180  
| | | | |  
Db 121 VVNVVYSSKDOARÖALDLKNGFÖLENTFLKVAIYPDEMAAQÖNPLÖQPRGRGIGÖRGSS 180  
OY 181 ROGSPGVSÖKÖPCDPLRLVPTÖFVGAIIÖKEGATIRNITÖKÖSIDVHÖKENAGAA 240  
| | | | |  
Db 181 ROGSPGVSÖKÖPCDPLRLVPTÖFVGAIIÖKEGATIRNITÖKÖSIDVHÖKENAGAA 240  
OY 241 EKSITILSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEÖIPLKILAHNNVÖGRLÖKEGRNLK 300  
| | | | |  
Db 241 EKSITILSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEÖIPLKILAHNNVÖGRLÖKEGRNLK 300  
OY 301 KÖEÖDTÖKÖITISPLÖÖELITLYNÖPERTÖTVKÖGNÖVÖTÖKAKABEÖIMKKIÖRESYENDÖIASMNL 360  
| | | | |  
Db 301 KÖEÖDTÖKÖITISPLÖÖELITLYNÖPERTÖTVKÖGNÖVÖTÖKAKABEÖIMKKIÖRESYENDÖIASMNL 360  
OY 361 ÖAHÖLIPÖGÖLNALÖGLFÖPTSGMÖPÖTSGPÖSÖMÖPPYÖPÖFÖSÖTÖETVÖHÖFÖIALSVGAI 420  
| | | | |  
Db 361 ÖAHÖLIPÖGÖLNALÖGLFÖPTSGMÖPÖTSGPÖSÖMÖPPYÖPÖFÖSÖTÖETVÖHÖFÖIALSVGAI 420

OY 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVWVITITGPEAOFKAGRIYKIKEENV 480  
| | | | |  
Db 421 IKGOGHITKOLSRFRAGASIKIAPAPADAKVWVITITGPEAOFKAGRIYKIKEENV 480  
OY 481 SPKEEVLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPVRDÖTPENDÖVVVKIT 540  
| | | | |  
Db 481 SPKEEVLEAHIRVPSFPAAGRVIGKGGKTVNEIÖNLSSAEVVPVRDÖTPENDÖVVVKIT 540  
OY 541 GHFYACVQAORRKIDIELITQYKOHQOKALOSGPPQSRK 579  
| | | | |  
Db 541 GHFYACVQAORRKIDIELITQYKOHQOKALOSGPPQSRK 579

## RESULT 13

US-09-735-705-176  
; Sequence 176, Application us/09735705  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaltanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: us/09/735.705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-176

Query Match 100.0%; Score 579; DB 21; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
| | | | |  
Db 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGYAFVDCPPDESMLKAIKIALSGK 60  
OY 61 IELHGKPIEVHSVPKROIRIKLOIRNIPHLÖMEVLDLSLVOYGVESECOYNTDSETA 120  
| | | | |  
Db 61 IELHGKPIEVHSVPKROIRIKLOIRNIPHLÖMEVLDLSLVOYGVESECOYNTDSETA 120  
OY 121 VVNVVYSSKDOARÖALDLKNGFÖLENTFLKVAIYPDEMAAQÖNPLÖQPRGRGIGÖRGSS 180  
| | | | |  
Db 121 VVNVVYSSKDOARÖALDLKNGFÖLENTFLKVAIYPDEMAAQÖNPLÖQPRGRGIGÖRGSS 180  
OY 181 ROGSPGVSÖKÖPCDPLRLVPTÖFVGAIIÖKEGATIRNITÖKÖSIDVHÖKENAGAA 240  
| | | | |  
Db 181 ROGSPGVSÖKÖPCDPLRLVPTÖFVGAIIÖKEGATIRNITÖKÖSIDVHÖKENAGAA 240  
OY 241 EKSITILSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEÖIPLKILAHNNVÖGRLÖKEGRNLK 300  
| | | | |  
Db 241 EKSITILSTPÖGTSACÖSILEIMHÖKEÖDÖKFTÖEÖIPLKILAHNNVÖGRLÖKEGRNLK 300  
OY 301 KÖEÖDTÖKÖITISPLÖÖELITLYNÖPERTÖTVKÖGNÖVÖTÖKAKABEÖIMKKIÖRESYENDÖIASMNL 360  
| | | | |  
Db 301 KÖEÖDTÖKÖITISPLÖÖELITLYNÖPERTÖTVKÖGNÖVÖTÖKAKABEÖIMKKIÖRESYENDÖIASMNL 360  
OY 361 ÖAHÖLIPÖGÖLNALÖGLFÖPTSGMÖPÖTSGPÖSÖMÖPPYÖPÖFÖSÖTÖETVÖHÖFÖIALSVGAI 420  
| | | | |  
Db 361 ÖAHÖLIPÖGÖLNALÖGLFÖPTSGMÖPÖTSGPÖSÖMÖPPYÖPÖFÖSÖTÖETVÖHÖFÖIALSVGAI 420

Qy	421	IKGQOQHITKQLSRAGASITKINAPADPAVVRNVITITGPEQKQAGRIYKIKEMENFV	480
Db	421	IKGQOQHITKQLSRAGASITKINAPADPAVVRNVITITGPEQKQAGRIYKIKEMENFV	480
Qy	421	IKGQOQHITKQLSRAGASITKINAPADPAVVRNVITITGPEQKQAGRIYKIKEMENFV	480
Db	421	IKGQOQHITKQLSRAGASITKINAPADPAVVRNVITITGPEQKQAGRIYKIKEMENFV	480
Qy	481	SRKEEVKLEAIRIPSPFAGRIYIGKGYVNELOINLSAEVYVPRDQTPENDQYVAVIT	540
Db	481	SRKEEVKLEAIRIPSPFAGRIYIGKGYVNELOINLSAEVYVPRDQTPENDQYVAVIT	540
Qy	481	SRKEEVKLEAIRIPSPFAGRIYIGKGYVNELOINLSAEVYVPRDQTPENDQYVAVIT	540
Db	481	SRKEEVKLEAIRIPSPFAGRIYIGKGYVNELOINLSAEVYVPRDQTPENDQYVAVIT	540
Qy	541	GHEFYACQYAAKCKIDIELITVYKHOQKRALDGGPDSRRK	579
Db	541	GHEFYACQYAAKCKIDIELITVYKHOQKRALDGGPDSRRK	579
Qy	541	GHEFYACQYAAKCKIDIELITVYKHOQKRALDGGPDSRRK	579
Db	541	GHEFYACQYAAKCKIDIELITVYKHOQKRALDGGPDSRRK	579

RESULT 14

```

US-09-791-537-49019
Sequence 49019, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 49019
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-49019

```

Query Match	100.0%	Score 579;	DB 21;	Length 579;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 579;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MKKLIGLSENAPADLSIPIKRAKIPVSGPPLYTVGCAVQDPDESNALKAIFALGK	60
Db	1	MKKLIGLSENAPADLSIPIKRAKIPVSGPPLYTVGCAVQDPDESNALKAIFALGK	60
Qy	61	IELHCKPIEVHSHVPSRKQIRIRLOLRNIPHLQMEVLBSLLVOYGAVSECOEYNIDSBTA	120
Db	61	IELHCKPIEVHSHVPSRKQIRIRLOLRNIPHLQMEVLBSLLVOYGAVSECOEYNIDSBTA	120
Qy	121	VYNYWYSSKQDARQALDKNGOLENTFLVVAITPEMAAQNLOQPRRRGLQBRSS	180
Db	121	VYNYWYSSKQDARQALDKNGOLENTFLVVAITPEMAAQNLOQPRRRGLQBRSS	180
Qy	181	RCGSGVGSXKQCDPLPYLWLPQFALITGEGATIRNTKQSGKIDYHREKMACAA	240
Db	181	RCGSGVGSXKQCDPLPYLWLPQFALITGEGATIRNTKQSGKIDYHREKMACAA	240
Qy	241	EXSTILSTPEGNSAACSEITFIMHKEADQIKTEBIPKLILANNVCHLIGKGRYUK	300
Db	241	EXSTILSTPEGNSAACSEITFIMHKEADQIKTEBIPKLILANNVCHLIGKGRYUK	300
Qy	301	KLEODTOKTITISPLQDELNLNPEKTIIVYGVNFTCAABEEIYKAKITREYENDIASNL	360
Db	301	KLEODTOKTITISPLQDELNLNPEKTIIVYGVNFTCAABEEIYKAKITREYENDIASNL	360
Qy	361	QMHILPGLNLNALGELPPSGMPPTSGPPSANTPPYQPOFQOSTETVHOPIALSVCAI	420
Db	361	QMHILPGLNLNALGELPPSGMPPTSGPPSANTPPYQPOFQOSTETVHOPIALSVCAI	420
Qy	421	ICKGQOHIKOLSRFACASIKTAPADADKAVRWVITIGPAPQKRAQRIYKIKENFV	480
Db	421	ICKGQOHIKOLSRFACASIKTAPADADKAVRWVITIGPAPQKRAQRIYKIKENFV	480
Qy	481	SPKEEYKLEAHIVPSPAGRIYICKGKTYNELQNLSSAEVYWRDQTPENDQYVVAIT	540
Db	481	SPKEEYKLEAHIVPSPAGRIYICKGKTYNELQNLSSAEVYWRDQTPENDQYVVAIT	540

Oy	541 GHHYACQVAQRKIDIELTVYQHQQOKALOSGPPQSRRK .579
Db	541 GHHYACQVAQRKIDIELTVYQHQQOKALSGPQSRRK .579

RESULT 15

```

US-09-850-716-176
Sequence 176, Application US/09850716
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Rether, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716-176

```

Query Match	100.0%	Score 579;	DB 22;	Length 579;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 579; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	MMKLTIGLUSNNAAPDLESIFKOAKITPVSGPLVYTCGVDDPDBSMYAKIAIHLGSK	60
Dd	1	MMKLTIGLUSNNAAPDLESIFKOAKITPVSGPLVYTCGVDDPDBSMYAKIAIHLGSK	60
Qy	61	TELHCKPIEVBHSPKROKIRIKLOIRINPHLOMEYDLSLVOYGVSECEYVNTDSETA	120
Dd	61	IELHCKPIEVBHSPKROKIRIKLOIRINPHLOMEYDLSLVOYGVSECEYVNTDSETA	120
Qy	121	VWNVYSSSKDARQALDKNLNGFOLNFTLKVAAIDPBNMAAOONLQOPRCRRLQGRSS	180
Dd	121	VWNVYSSSKDARQALDKNLNGFOLNFTLKVAAIDPBNMAAOONLQOPRCRRLQGRSS	180
Qy	181	RGSGSGSVKOKKCDPLRLVLYPPOFGALITGEGATIRINTKOTGSKIDVHNKKENAGAA	240
Dd	181	RGSGSGSVKOKKCDPLRLVLYPPOFGALITGEGATIRINTKOTGSKIDVHNKKENAGAA	240
Qy	241	EKSTITLSTEGSAAKCSLEIEMHKKAODIKTEEIPKLTILAHNNVGLJGKBGRYLK	300
Dd	241	EKSTITLSTEGSAAKCSLEIEMHKKAODIKTEEIPKLTILAHNNVGLJGKBGRYLK	300
Qy	301	KTEODPTDKITTIPLDLELTVNPERTITVYGNVETCAKAEEIIMKKTRESYENDIASNML	360
Dd	301	KTEODPTDKITTIPLDLELTVNPERTITVYGNVETCAKAEEIIMKKTRESYENDIASNML	360
Qy	361	QAHILPGLNINNALGPEPPSGMPPTSGPSAMTPYPOFOFOSCTEYVHOETIPALSVCAI	420
Dd	361	QAHILPGLNINNALGPEPPSGMPPTSGPSAMTPYPOFOFOSCTEYVHOETIPALSVCAI	420
Qy	421	IKGOGQHKOLSTFPAKASAKIAPAPADAKVVRVYITGPAPAOQKAOGRTYKIKKEENFV	480
Dd	421	IKGOGQHKOLSTFPAKASAKIAPAPADAKVVRVYITGPAPAOQKAOGRTYKIKKEENFV	480
Qy	481	SPKEBVKLEAHIVNVPFAAGAVITKGGKTVNELOINLSAEEVVYVRDPTDPENDQVVAVIT	540
Dd	481	SPKEBVKLEAHIVNVPFAAGAVITKGGKTVNELOINLSAEEVVYVRDPTDPENDQVVAVIT	540

Db 481 SPKEEVKLEAHIRVPSPFAGRVIGKSGKTVNELQNLSAEVVPFRDPTDPENDOVVVKIT 540

OY 541 GHFYACQVAQRKIOEILITQYKHQOQKALQSGPPQSRK 579

Db 541 GHFYACQVAQRKIOEILITQYKHQOQKALQSGPPQSRK 579

Search completed: April 16, 2003, 16:45:11  
Job time : 395.655 secs





Qy 361 QAHLLPGMLNMLGLFPTSGMPPTSGPPSAMTPPYPOFOSSETETVHOFLPALSVGAI 420  
Db 361 QAHLLPGMLNMLGLFPTSGMPPTSGPPSAMTPPYPOFOSSETETVHOFLPALSVGAI 420  
Qy 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480  
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQMLSSAEVYVVRDTPENDQVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQMLSSAEVYVVRDTPENDQVYVKIT 540  
Qy 541 GHFYACQVAKRKIDELITVYKHOHQOKKALQSGPPOSRRK 579  
Db 541 GHFYACQVAKRKIDELITVYKHOHQOKKALQSGPPOSRRK 579

RESULT 2  
US-10-348-119-255

Sequence 255, Application US/10348119  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING  
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE  
FILE REFERENCE: D0185 NP  
CURRENT APPLICATION NUMBER: US/10/348,119  
PRIOR FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US 60/350,061  
NUMBER OF SEQ ID NOS: 795  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 255  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-348-119-255

## Query Match 100.0%; Score 579; DB 6; Length 579;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMALKAIEMLSGK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMALKAIEMLSGK 60  
Qy 61 IELHGRPIEVESHVYKROIRIKLQIRNIPPHQWELVDSLVOYGVSECEQVNTDSETA 120  
Db 61 IELHGRPIEVESHVYKROIRIKLQIRNIPPHQWELVDSLVOYGVSECEQVNTDSETA 120  
Qy 121 VVAVTSSKQARQALDKLNGFOLNFETLKVAIIPDEMAAQONPLQOPRGRGLGRCSS 180  
Db 121 VVAVTSSKQARQALDKLNGFOLNFETLKVAIIPDEMAAQONPLQOPRGRGLGRCSS 180  
Qy 181 RQSPGSVSKORPCDPLRLVLVPOFGAIIKKEGATIRNTTKOTOSKIDVHKKENAGAA 240  
Db 181 RQSPGSVSKORPCDPLRLVLVPOFGAIIKKEGATIRNTTKOTOSKIDVHKKENAGAA 240  
Qy 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEEIPLKILLANNFVGLIKKEGRNLK 300  
Db 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEEIPLKILLANNFVGLIKKEGRNLK 300  
Qy 301 KIEQDPTDKITITSPLOETLYNPERTITVKGAVETCAKAEIEIKKIRESEYENDIASNML 360  
Db 301 KIEQDPTDKITITSPLOETLYNPERTITVKGAVETCAKAEIEIKKIRESEYENDIASNML 360  
Qy 361 QAHLLPGMLNMLGLFPTSGMPPTSGPPSAMTPPYPOFOSSETETVHOFLPALSVGAI 420  
Db 361 QAHLLPGMLNMLGLFPTSGMPPTSGPPSAMTPPYPOFOSSETETVHOFLPALSVGAI 420  
Qy 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480  
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480

Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQMLSSAEVYVVRDTPENDQVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQMLSSAEVYVVRDTPENDQVYVKIT 540  
Qy 541 GHFYACQVAKRKIDELITVYKHOHQOKKALQSGPPOSRRK 579  
Db 541 GHFYACQVAKRKIDELITVYKHOHQOKKALQSGPPOSRRK 579

## RESULT 3

US-09-724-676-92918

Sequence 92918, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92918

## Query Match 95.5%; Score 553; DB 5; Length 558;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMALKAIEMLSGK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPELVKTGYAFVDCPDDESMALKAIEMLSGK 60  
Qy 61 IELHGRPIEVESHVYKROIRIKLQIRNIPPHQWELVDSLVOYGVSECEQVNTDSETA 120  
Db 61 IELHGRPIEVESHVYKROIRIKLQIRNIPPHQWELVDSLVOYGVSECEQVNTDSETA 120  
Qy 121 VVAVTSSKQARQALDKLNGFOLNFETLKVAIIPDEMAAQONPLQOPRGRGLGRCSS 180  
Db 121 VVAVTSSKQARQALDKLNGFOLNFETLKVAIIPDEMAAQONPLQOPRGRGLGRCSS 180  
Qy 181 RQSPGSVSKORPCDPLRLVLVPOFGAIIKKEGATIRNTTKOTOSKIDVHKKENAGAA 240  
Db 181 RQSPGSVSKORPCDPLRLVLVPOFGAIIKKEGATIRNTTKOTOSKIDVHKKENAGAA 240  
Qy 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEEIPLKILLANNFVGLIKKEGRNLK 300  
Db 241 EKSIITLSTPECTSAACKSILEIMHKEADIKFTEEIPLKILLANNFVGLIKKEGRNLK 300  
Qy 301 KIEQDPTDKITITSPLOETLYNPERTITVKGAVETCAKAEIEIKKIRESEYENDIASNML 360  
Db 301 KIEQDPTDKITITSPLOETLYNPERTITVKGAVETCAKAEIEIKKIRESEYENDIASNML 360  
Qy 361 QAHLLPGMLNMLGLFPTSGMPPTSGPPSAMTPPYPOFOSSETETVHOFLPALSVGAI 420  
Db 361 QAHLLPGMLNMLGLFPTSGMPPTSGPPSAMTPPYPOFOSSETETVHOFLPALSVGAI 420  
Qy 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480  
Db 421 IKGOGHIKQLSRFAGASIKIAPAEAPDAKVMVITITGPPEAKOAGRIYGIKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQMLSSAEVYVVRDTPENDQVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGAGVIGKGGKTVNELQMLSSAEVYVVRDTPENDQVYVKIT 540  
Qy 541 GHFYACQVAKRK 553  
Db 541 GHFYACQVAKRK 553



```
RESULT 4
US-09-724-676A-92918
; Sequence 92918, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-724-676A-92918
```

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Query Match          95.5%; Score 553; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGAFVDCPDDESMALKATEALS60
DB 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGAFVDCPDDESMALKATEALS60
QY 61 IELHGKPIEVEHSPVKRQIRKLOIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSE7A 120
DB 61 IELHGKPIEVEHSPVKRQIRKLOIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSE7A 120
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
DB 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
DB 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
QY 181 RQSGSGSVSKQKPCDPLRLVPTQFVGALIGEGATIRNITQOTQSKIDVHRKENAGAA 240
DB 181 RQSGSGSVSKQKPCDPLRLVPTQFVGALIGEGATIRNITQOTQSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGLIGEGRN1K 300
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGLIGEGRN1K 300
QY 301 KIEODTDTKITISPLQELTYNPERTITVKGAVETCAKAEEMKIRIERYENDIASMNL 360
DB 301 KIEODTDTKITISPLQELTYNPERTITVKGAVETCAKAEEMKIRIERYENDIASMNL 360
QY 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETETVHOFTIPALSVGAI 420
DB 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETETVHOFTIPALSVGAI 420
QY 421 IKGQGHIKOLSRFAGASIKIAPAEAPDAKVRMYIITGPPEAQFKAQRIYGIKEENFV 480
DB 421 IKGQGHIKOLSRFAGASIKIAPAEAPDAKVRMYIITGPPEAQFKAQRIYGIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQMLSSAEVVPDPDQTPDENDQVVA7TT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQMLSSAEVVPDPDQTPDENDQVVA7TT 540
QY 541 GHFYACQVAQRKI 553
DB 541 GHFYACQVAQRKI 553
```

```
RESULT 5
US-09-724-676-92916
; Sequence 92916, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-724-676-92916
```

```
Query Match          80.7%; Score 467; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGAFVDCPDDESMALKATEALS60
DB 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGAFVDCPDDESMALKATEALS60
QY 61 IELHGKPIEVEHSPVKRQIRKLOIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSE7A 120
DB 61 IELHGKPIEVEHSPVKRQIRKLOIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSE7A 120
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
DB 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
DB 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
QY 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGLIGEGRN1K 300
DB 241 EKSTITLSTPEGSTSAACKSILEIMHKEADIKFTEIPLKILAHNPFVGLIGEGRN1K 300
QY 301 KIEODTDTKITISPLQELTYNPERTITVKGAVETCAKAEEMKIRIERYENDIASMNL 360
DB 301 KIEODTDTKITISPLQELTYNPERTITVKGAVETCAKAEEMKIRIERYENDIASMNL 360
QY 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETETVHOFTIPALSVGAI 420
DB 361 QAHLIPGLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQETETVHOFTIPALSVGAI 420
QY 421 IKGQGHIKOLSRFAGASIKIAPAEAPDAKVRMYIITGPPEAQFKAQRIYGIKEENFV 480
DB 421 IKGQGHIKOLSRFAGASIKIAPAEAPDAKVRMYIITGPPEAQFKAQRIYGIKEENFV 480
```

```
RESULT 6
US-09-724-676A-92916
; Sequence 92916, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-724-676A-92916
```

```
Query Match          80.7%; Score 467; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGAFVDCPDDESMALKATEALS60
DB 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPLVKTGAFVDCPDDESMALKATEALS60
QY 61 IELHGKPIEVEHSPVKRQIRKLOIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSE7A 120
DB 61 IELHGKPIEVEHSPVKRQIRKLOIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSE7A 120
QY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKVAVIPDEMAAQNPLQOPRGRGLGGRGSS 180
```

```
|||||
Db 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRRRRLGGRSS 180
QY 181 RQSGPGSVSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHKENAGA 240
Db 181 RQSGPGSVSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHKENAGA 240
QY 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEIEPLKTLANNFVGRILGKERNLK 300
Db 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEIEPLKTLANNFVGRILGKERNLK 300
QY 301 KIEODPTKITISPLQELLYNPERTIYKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEODPTKITISPLQELLYNPERTIYKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
QY 361 QAHILPGLINNALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
Db 361 QAHILPGLINNALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPAOQKQ 467
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPAOQKQ 467

RESULT 7
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 579
; TYPE: PRN
; ORGANISM: primate
US-10-313-986-484
```

```
Query Match 68.7%; Score 398; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 NAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGETELHGRPIEVE 71
Db 12 NAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGETELHGRPIEVE 71
QY 72 HSVKRRORIRKQIRINIPHLOWEVLDSLVOYGVESCEQVNTSETAVVNTYSSKQ 131
Db 72 HSVKRRORIRKQIRINIPHLOWEVLDSLVOYGVESCEQVNTSETAVVNTYSSKQ 131
QY 132 ARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRRRRLGGRSSRQSGPGSVSKQ 191
Db 132 ARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRRRRLGGRSSRQSGPGSVSKQ 191
QY 192 KPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHKENAGAESTIILSTPE 251
Db 192 KPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHKENAGAESTIILSTPE 251
QY 252 GTSACKSILEIMHKEADIKFTEIEPLKTLANNFVGRILGKERNLKIEODPTKIT 311
Db 252 GTSACKSILEIMHKEADIKFTEIEPLKTLANNFVGRILGKERNLKIEODPTKIT 311
QY 312 ISPIQELTYNPERTIYKGNVETCAKAEIEIMKKIRESYENDIASMNLQAHILPOLN 371
Db 312 ISPIQELTYNPERTIYKGNVETCAKAEIEIMKKIRESYENDIASMNLQAHILPOLN 371
```

```
QY 372 ALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVH 409
Db 372 ALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVH 409

RESULT 8
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-313-986-348
```

```
Query Match 65.1%; Score 377; DB 6; Length 579;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGET 60
Db 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKATEALSGET 60
QY 61 IELHGRPIEVEHSVPRORIRKQIRINIPHLOWEVLDSLVOYGVESCEQVNTSETA 120
Db 61 IELHGRPIEVEHSVPRORIRKQIRINIPHLOWEVLDSLVOYGVESCEQVNTSETA 120
QY 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRRRRLGGRSS 180
Db 121 VVNVYSSKQDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRRRRLGGRSS 180
QY 181 RQSGPGSVSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHKENAGA 240
Db 181 RQSGPGSVSKQKPCDPLRLVPTQFVGAIIGKEGATIRNTKOTOSKIDVHKENAGA 240
QY 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEIEPLKTLANNFVGRILGKERNLK 300
Db 241 EKSTIILSTPGTSAACKSILEIMHKEADIKFTEIEPLKTLANNFVGRILGKERNLK 300
QY 301 KIEODPTKITISPLQELLYNPERTIYKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEODPTKITISPLQELLYNPERTIYKGNVETCAKAEIEIMKKIRESYENDIASMNL 360
QY 361 QAHILPGLINNALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
Db 361 QAHILPGLINNALGLPPTSGMPPTSGPPSAMTPPYPOFQOSETEVHOIFALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPAOQKQAGRIYKKEENFV 480
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPAOQKQAGRIYKKEENFV 480
QY 481 SPKEVEVLHNIHVPSFAGRIYIGGKTVNELNLSAEVYVPRODTPENDQVYVKT 540
Db 481 SPKEVEVLHNIHVPSFAGRIYIGGKTVNELNLSAEVYVPRODTPENDQVYVKT 540
QY 541 GHFACQVAAQRKIOELITVOYKHOQKALQSGPPQSRK 579
Db 541 GHFACQVAAQRKIOELITVOYKHOQKALQSGPPQSRK 579
```

## RESULT 9

US-10-313-986-446  
 ; Sequence 446, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C19  
 ; CURRENT APPLICATION NUMBER: US/10/313.986  
 ; CURRENT FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 560  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 446  
 ; LENGTH: 579  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-313-986-446

Query Match 65.1%; Score 377; DB 6; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFVDCPPESWALKAIEALSGK 60  
 DB 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFVDCPPESWALKAIEALSGK 60  
 QY 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELDSLVOYGVESEQVNTDSETA 120  
 DB 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELDSLVOYGVESEQVNTDSETA 120  
 QY 121 VVNVYSSKDQARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLOQPRGRGLGGRSS 180  
 DB 121 VVNVYSSKDQARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLOQPRGRGLGGRSS 180  
 QY 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 DB 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 QY 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPILKILAHNNEVGLICEGRNKK 300  
 DB 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPILKILAHNNEVGLICEGRNKK 300  
 QY 301 KIEQDTDKITISPLQELTLNPERTITVKGNETCAKAEELIMKTIRESYENDIASMNL 360  
 DB 301 KIEQDTDKITISPLQELTLNPERTITVKGNETCAKAEELIMKTIRESYENDIASMNL 360  
 QY 361 QAHILPGNLNALGLPPTSGMPPTSGPSAMTPPYPOEJSETETVHOFIPALSVGAI 420  
 DB 361 QAHILPGNLNALGLPPTSGMPPTSGPSAMTPPYPOEJSETETVHOFIPALSVGAI 420  
 QY 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 DB 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSSAEVVPVROTDENDQVVKIT 540  
 DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSSAEVVPVROTDENDQVVKIT 540  
 QY 541 GHFYACQVAQRKIOEILTVQKHQOKALOSGPQSRKK 579  
 DB 541 GHFYACQVAQRKIOEILTVQKHQOKALOSGPQSRKK 579

## RESULT 10

US-10-313-986-449  
 ; Sequence 449, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C19  
 ; CURRENT APPLICATION NUMBER: US/10/313.986  
 ; CURRENT FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 560  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 449  
 ; LENGTH: 579  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-313-986-449

Query Match 65.1%; Score 377; DB 6; Length 579;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFVDCPPESWALKAIEALSGK 60  
 DB 1 MNKLYIGLSENAPSDLESIFKDAKIPVSGPLVKTGVAFVDCPPESWALKAIEALSGK 60  
 QY 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELDSLVOYGVESEQVNTDSETA 120  
 DB 61 IELHCKPIEVHSHVKKRRIKLOIRNIPHLQWELDSLVOYGVESEQVNTDSETA 120  
 QY 121 VVNVYSSKDQARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLOQPRGRGLGGRSS 180  
 DB 121 VVNVYSSKDQARQALDKLNGFQLENFTLVAVYIPDEMAAQNPLOQPRGRGLGGRSS 180  
 QY 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 DB 181 RQSGSVSKKPCDPLRLVPTQFVGAITGEGATIRNTKOTOSKIDVHKENAGAA 240  
 QY 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPILKILAHNNEVGLICEGRNKK 300  
 DB 241 EKSITILSTPGTSAACKSILEIMHKEADIKFTEEIPILKILAHNNEVGLICEGRNKK 300  
 QY 301 KIEQDTDKITISPLQELTLNPERTITVKGNETCAKAEELIMKTIRESYENDIASMNL 360  
 DB 301 KIEQDTDKITISPLQELTLNPERTITVKGNETCAKAEELIMKTIRESYENDIASMNL 360  
 QY 361 QAHILPGNLNALGLPPTSGMPPTSGPSAMTPPYPOEJSETETVHOFIPALSVGAI 420  
 DB 361 QAHILPGNLNALGLPPTSGMPPTSGPSAMTPPYPOEJSETETVHOFIPALSVGAI 420  
 QY 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 DB 421 IKGQOHKOLSRFAGASIKIAPAEAPDAKVRMYITGPPEAOPKAGRIYGIKEENFY 480  
 QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSSAEVVPVROTDENDQVVKIT 540  
 DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTYNELONLSSAEVVPVROTDENDQVVKIT 540  
 QY 541 GHFYACQVAQRKIOEILTVQKHQOKALOSGPQSRKK 579  
 DB 541 GHFYACQVAQRKIOEILTVQKHQOKALOSGPQSRKK 579

## RESULT 11

US-10-313-986-480  
 ; Sequence 480, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C19

```

: CURRENT APPLICATION NUMBER: US/10/313.986
: CURRENT FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 560
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 480
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-313-986-480
```

```

Query Match          65.1%; Score 377; DB 6; Length 579;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 MNKLYIGLSENAPSDLESTIFKDAKIPVSGPIVKTGYAVVDCPDDESMALKATEALSGK 60
DB 1 MNKLYIGLSENAPSDLESTIFKDAKIPVSGPIVKTGYAVVDCPDDESMALKATEALSGK 60
QY 61 IELHCKPIEVEHSVKKRRIKRLQIRNIPHLQWEYLSLVOYGVESECVQVNTDSETA 120
DB 61 IELHCKPIEVEHSVKKRRIKRLQIRNIPHLQWEYLSLVOYGVESECVQVNTDSETA 120
QY 121 VVNVITYSSKDAQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRLGORGSS 180
DB 121 VVNVITYSSKDAQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRLGORGSS 180
QY 181 ROGSGSVSKOKPCDPLRLVPTQFVGATIGKEGATIRNITKOTQSKIDVHRKEMGAA 240
DB 181 ROGSGSVSKOKPCDPLRLVPTQFVGATIGKEGATIRNITKOTQSKIDVHRKEMGAA 240
QY 241 EKSTITLSPREGTSACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGKEGNL 300
DB 241 EKSTITLSPREGTSACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGKEGNL 300
QY 301 KIQODPTDKITISPLQELTLNPERTTVKGNVETCAKAEEMIMKIRESEENDIASMNL 360
DB 301 KIQODPTDKITISPLQELTLNPERTTVKGNVETCAKAEEMIMKIRESEENDIASMNL 360
QY 361 QAHILPGLNMLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420
DB 361 QAHILPGLNMLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPADAPAKYRVYITGPPEAOFKAGRIYKIKENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPADAPAKYRVYITGPPEAOFKAGRIYKIKENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGYVNEIQLNLSAEVYVPRDQTPDENDVYVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRYIGKGYVNEIQLNLSAEVYVPRDQTPDENDVYVKIT 540
QY 541 GHFYACQVAVORKIOELITLQVKKHQQOKALQSGPQSRK 579
DB 541 GHFYACQVAVORKIOELITLQVKKHQQOKALQSGPQSRK 579
```

```

RESULT 12
US-10-313-986-486
: Sequence 486, Application US/10313986
: GENERAL INFORMATION:
: APPLICANT: Foy, Teresa M.
: APPLICANT: McNabb, Andria
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Reed, Steven G.
: APPLICANT: Wang, Tonglong
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C19
: CURRENT APPLICATION NUMBER: US/10/313.986
: CURRENT FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 560
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 486
: LENGTH: 589
```

```

: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-313-986-486
```

```

Query Match          65.1%; Score 377; DB 6; Length 589;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 MNKLYIGLSENAPSDLESTIFKDAKIPVSGPIVKTGYAVVDCPDDESMALKATEALSGK 60
DB 1 MNKLYIGLSENAPSDLESTIFKDAKIPVSGPIVKTGYAVVDCPDDESMALKATEALSGK 60
QY 61 IELHCKPIEVEHSVKKRRIKRLQIRNIPHLQWEYLSLVOYGVESECVQVNTDSETA 120
DB 61 IELHCKPIEVEHSVKKRRIKRLQIRNIPHLQWEYLSLVOYGVESECVQVNTDSETA 120
QY 121 VVNVITYSSKDAQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRLGORGSS 180
DB 121 VVNVITYSSKDAQALDKLNGFOLNFTLKVAIIPDEMAAQNPLQOPRGRRLGORGSS 180
QY 181 ROGSGSVSKOKPCDPLRLVPTQFVGATIGKEGATIRNITKOTQSKIDVHRKEMGAA 240
DB 181 ROGSGSVSKOKPCDPLRLVPTQFVGATIGKEGATIRNITKOTQSKIDVHRKEMGAA 240
QY 241 EKSTITLSPREGTSACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGKEGNL 300
DB 241 EKSTITLSPREGTSACKSILEIMHKEADIKFTEIPLKILAHNNFVGRILGKEGNL 300
QY 301 KIQODPTDKITISPLQELTLNPERTTVKGNVETCAKAEEMIMKIRESEENDIASMNL 360
DB 301 KIQODPTDKITISPLQELTLNPERTTVKGNVETCAKAEEMIMKIRESEENDIASMNL 360
QY 361 QAHILPGLNMLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420
DB 361 QAHILPGLNMLNLGLPPTSGMPPTSGPSAMTPPYPOESESIEYHOFIPALSYGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPADAPAKYRVYITGPPEAOFKAGRIYKIKENFV 480
DB 421 IKGOGHITKOLSRFAGASIKIAPADAPAKYRVYITGPPEAOFKAGRIYKIKENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRYIGKGYVNEIQLNLSAEVYVPRDQTPDENDVYVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRYIGKGYVNEIQLNLSAEVYVPRDQTPDENDVYVKIT 540
QY 541 GHFYACQVAVORKIOELITLQVKKHQQOKALQSGPQSRK 579
DB 541 GHFYACQVAVORKIOELITLQVKKHQQOKALQSGPQSRK 579
```

```

RESULT 13
US-10-313-986-427
: Sequence 427, Application US/10313986
: GENERAL INFORMATION:
: APPLICANT: Foy, Teresa M.
: APPLICANT: McNabb, Andria
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Reed, Steven G.
: APPLICANT: Wang, Tonglong
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C19
: CURRENT APPLICATION NUMBER: US/10/313.986
: CURRENT FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 560
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 427
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-313-986-427
```

```

Query Match          64.9%; Score 376; DB 6; Length 586;
Best Local Similarity 99.7%; Pred. No. 0;
```

Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 2 NKLTYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSSMLKAIKIALSGK 61
    |||
DB 9 NKLTYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSSMLKAIKIALSGK 68
    |||
OY 62 ELHGKPIEVEHSVPKRQRIKLOIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7AV 121
    |||
DB 69 ELHGKPIEVEHSVPKRQRIKLOIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7AV 128
    |||
OY 122 VVNTYSSKDQARQALDKLNGFOLNFTLKAYIIPDEMAAQNLOQPRGRGIGOGSSR 181
    |||
DB 129 VVNTYSSKDQARQALDKLNGFOLNFTLKAYIIPDEMAAQNLOQPRGRGIGOGSSR 188
    |||
OY 182 QGSPGVSVKQKPCDLPRLPLPTQVGAIGKSGATIRNTKOTQSKIDVHRKENGAGAE 241
    |||
DB 189 QGSPGVSVKQKPCDLPRLPLPTQVGAIGKSGATIRNTKOTQSKIDVHRKENGAGAE 248
    |||
OY 242 KSTITLSTPECTSAACKSILEIMHKEKODIKFTEELPLKILAHNNFVGRIGKEGNLKK 301
    |||
DB 249 KSTITLSTPECTSAACKSILEIMHKEKODIKFTEELPLKILAHNNFVGRIGKEGNLKK 308
    |||
OY 302 IEODDTKITTSPLQELTIVNPERTIVKGNVETCAKAEIEIMKTIRESYENDIASMNIO 361
    |||
DB 309 IEODDTKITTSPLQELTIVNPERTIVKGNVETCAKAEIEIMKTIRESYENDIASMNIO 368
    |||
OY 362 AHLIPGLMLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFTPLASGATII 421
    |||
DB 369 AHLIPGLMLNLGLFPPTSGMPPTSGPPSAMTPPYPOFQOSETETVHOFTPLASGATII 428
    |||
OY 422 GKOGCHIKOLSRFAGASIKIAPAPADAKVMVITTPPAOPKAGORITGKIKENEFVS 481
    |||
DB 429 GKOGCHIKOLSRFAGASIKIAPAPADAKVMVITTPPAOPKAGORITGKIKENEFVS 488
    |||
OY 482 PKEVKLEAHRVSPFAGRTYKGTYNELNLSAEVYVPRDQTPDENOVVYKRTG 541
    |||
DB 489 PKEVKLEAHRVSPFAGRTYKGTYNELNLSAEVYVPRDQTPDENOVVYKRTG 548
    |||
OY 542 HFYACOVAKRKIOELITOVKOHOKALQSGPPQSRKK 579
    |||
DB 549 HFYACOVAKRKIOELITOVKOHOKALQSGPPQSRKK 586
    |||

```

RESULT 14  
US-09-724-676-92917

; Sequence 92917, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92917

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676-92917

Query Match 23.1%; Score 134; DB 5; Length 134;

Best Local Similarity 100.0%; Pred. No. 8,4e-129;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNKLYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSSMLKAIKIALSGK 60
    |||
DB 1 MNKLYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSSMLKAIKIALSGK 60
    |||
OY 61 ELHGKPIEVEHSVPKRQRIKLOIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120
    |||
DB 61 ELHGKPIEVEHSVPKRQRIKLOIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120
    |||
OY 121 VVNTYSSKDQARQ 134

```

DB 121 VVNTYSSKDQARQ 134

RESULT 15  
US-09-724-676A-92917

; Sequence 92917, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 92917

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676A-92917

Query Match 23.1%; Score 134; DB 5; Length 134;

Best Local Similarity 100.0%; Pred. No. 8,4e-129;

Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNKLYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSSMLKAIKIALSGK 60
    |||
DB 1 MNKLYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSSMLKAIKIALSGK 60
    |||
OY 61 ELHGKPIEVEHSVPKRQRIKLOIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120
    |||
DB 61 ELHGKPIEVEHSVPKRQRIKLOIRNIPPHLOMEVLDLSLVGYVSECEQVNTDSE7A 120
    |||
OY 121 VVNTYSSKDQARQ 134
    |||
DB 121 VVNTYSSKDQARQ 134
    |||

```

Search completed: April 16, 2003, 16:47:24

Job time: 121.793 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:31:34 ; Search time 37.0788 Seconds  
(without alignments)  
1501.176 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579  
Sequence: 1 MNKLYIGNLSENAPSDLES.....VKHQOQKALQSGPPQSRK 579

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: PIR-73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.4	242	2	G96994
2	8	1.4	311	2	A38558
3	8	1.4	324	2	AC0088
4	8	1.4	338	2	D95292
5	8	1.4	925	2	T02811
6	8	1.4	997	2	T43523
7	8	1.4	1000	2	S44898
8	8	1.4	1101	2	G70951
9	8	1.4	1198	2	B88279
10	8	1.4	1220	2	T19117
11	8	1.4	1472	2	B54774
12	8	1.4	1529	2	A59189
13	8	1.4	1704	2	S73163
14	8	1.4	1704	2	A59188
15	8	1.4	2201	2	AS3774
16	8	1.4	3164	1	WMBE66
17	8	1.2	59	2	D84234
18	7	1.2	76	2	A11993
19	7	1.2	107	2	B72498
20	7	1.2	121	2	T47741
21	7	1.2	123	2	D71922
22	7	1.2	123	2	H64592
23	7	1.2	130	2	T50778
24	7	1.2	132	2	F97592
25	7	1.2	132	2	AB2814
26	7	1.2	139	1	B69486
27	7	1.2	146	1	R5BSL5
28	7	1.2	153	1	HHSY17
29	7	1.2	170	2	G75043

30	7	1.2	182	2	B35650	hypothetical 20k p
31	7	1.2	183	2	S56460	probable alpha hel
32	7	1.2	183	2	C91280	probable alpha hel
33	7	1.2	183	2	C68121	probable alpha hel
34	7	1.2	183	2	AD1056	conserved hypother
35	7	1.2	185	2	C71117	hypothetical prote
36	7	1.2	192	2	A72646	hypothetical prote
37	7	1.2	203	2	UC6113	meatocyte-specific
38	7	1.2	232	2	G70738	probable PPE prote
39	7	1.2	239	1	D41316	flagellin B3 precu
40	7	1.2	239	2	G87265	conserved hypother
41	7	1.2	242	2	F87687	nucleotidyltransfe
42	7	1.2	279	2	T33429	hypothetical prote
43	7	1.2	285	2	T18689	hypothetical prote
44	7	1.2	286	2	F5104	hypothetical 31.3
45	7	1.2	286	2	C91132	hypothetical prote

#### ALIGNMENTS

RESULT 1  
G96994  
glycerol uptake facilitator protein, permease [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: G96994  
R:Noiling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: G96994  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-242 <R>  
A:Cross-references: 1-AE001437; PIDN:AAK78746.1; PID:G15023655; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0770  
C:Superfamily: glycerol facilitator protein

Query Match 1.4% Score 8; DB 2; Length 242;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 QFVGATIG 212  
DB 94 QFVGATIG 101

RESULT 2  
A38558  
interferon response element-binding factor 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 05-Nov-1999  
C:Accession: A38558  
R:Ryan, C.; Tamm, I.  
Proc. Natl. Acad. Sci. U.S.A. 89, 144-148, 1991  
A:Title: Molecular cloning and characterization of interferon alpha/beta response e  
A:Reference number: A38558; MUID:91095416; PMID:1986360  
A:Accession: A38558  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-311 <Y>  
A:Cross-references: GB:M55290; NID:G194096; PIDN:AAA37884.1; PID:G194097  
C:Keywords: DNA binding; phosphoprotein; transcription regulation

Query Match 1.4% Score 8; DB 2; Length 311;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 MNKLYIGNL 9





## RESULT 7

S44898 ZK1236.3 protein - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001

C:Accession: S44898

R:Ravello, A.D.

A:Submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the *C. elegans* cosmid ZK1236.

A:Reference number: S44622

A:Accession: S44898

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1000 &lt;FAV&gt;

A:Cross-references: EMBL:L13200; NID:g289748; PID:g289754

C:Genetics:

A:Introns: 56/3; 86/2; 189/3; 243/2; 669/3; 808/3; 984/3

Query Match

Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 PSDLESTF 22

Db 568 PSDLESTF 575

## RESULT 8

G70951 probable ATP-dependent DNA helicase - *Mycobacterium tuberculosis* (strain H37RV)C:Species: *Mycobacterium tuberculosis*

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: G70951

R:COLE, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulistio, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: G70951

A&gt;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1101 &lt;COL&gt;

A:Cross-references: GB:AL021646; GB:AL123456; NID:g3242278; PIDN:CAA16666.1; PID:el24879

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV3201c

Query Match

Best Local Similarity 100.0%; Pred. No. 31;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 ALGLPPT 379

Db 18 ALGLPPT 25

## RESULT 9

B88279 protein C08H9.2 (imported) - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001

C:Accession: B88279

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A:Reference number: A75000; PMID:99069613; PMID:9851916

A:Note: see webistes genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1198 &lt;STO&gt;

A:Cross-references: GB:chr\_II; PIDN:CAA91144.1; PID:g37874123; GSPDB:GN00020; CESP:C08

C:Genetics:

A:Gene: C08H9.2

A:Map position: 2

C:Superfamily: vlg11ln

Query Match

Best Local Similarity 100.0%; Pred. No. 34;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 289 GRIGKEG 296

Db 126 GRIGKEG 133

## RESULT 10

T19117 hypothetical protein C08H9.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T19117

R:DLOYD, C.

A:Submitted to the EMBL Data Library, October 1995

A:Reference number: Z19074

A:Accession: T19117

A&gt;Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1220 &lt;MTL&gt;

A:Cross-references: EMBL:Z54342; PIDN:CAA91144.2; GSPDB:GN00020; CESP:C08H9.2

A:Experimental source: clone C08H9

C:Genetics:

A:Gene: CESP:C08H9.2

A:Map position: 2

A:Introns: 7/1; 560/3; 949/3; 1155/3

C:Superfamily: vlg11ln

Query Match

Best Local Similarity 100.0%; Pred. No. 34;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 289 GRIGKEG 296

Db 148 GRIGKEG 155

## RESULT 11

B54774 ATP binding cassette transporter ABC2 - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Feb-2001

C:Accession: B54774

R:Luciani, M.F.; Denicourt, F.; Savary, S.; Mattei, M.G.; Chinini, G.

Genomics 21, 150-159, 1994

A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.

A:Reference number: A54774; PMID:94375008; PMID:8088782

A:Accession: B54774

A:Molecule type: mRNA

A:Residues: 1-1472 &lt;LUC&gt;

A:Cross-references: GB:X75927; NID:g495258; PIDN:CAA53531.1; PID:g495259

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

C:Keywords: ATP; nucleotide binding; P-loop

F:4-234/Domain: ATP-binding cassette homology &lt;ABC1&gt;

F:61-68/Region: nucleotide-binding motif A (P-loop)

F:1108-1300/Domain: ATP-binding cassette homology &lt;ABC2&gt;

F:1126-1133/Region: nucleotide-binding motif A (P-loop)

Query Match

Best Local Similarity 100.0%; Pred. No. 40;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 11111111  
 Db 76 GLEPPTSG 83

## RESULT 12

A59189  
 ATP-binding cassette transporter - human (fragment)  
 N:Alternate names: KIAA1062 protein  
 C:Species: Homo sapiens (man)  
 C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 02-Jun-2000  
 C:Accession: A59189  
 R:Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirose, M.; Miyajima, N.; Tanaka, A.; Kotani, DNA Res. 6, 197-205, 1999  
 A:Title: Prediction of the coding sequences of unidentified human genes. XIV. The complete  
 A:Reference number: 222961; MIM:99397452; PMID:10470851  
 A:Accession: A59189  
 A:Status: preliminary: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1529 <K1K>  
 A:Cross-references: GB:AB028985; NID:q5689460; PIDN:BA83014.1; PID:dl046841; PID:q56894  
 A:Experimental source: chromosome 9; clone hJ03579; clone 11b p19nescriptII SK plus; t1a  
 C:Genetics:  
 A:Map position: 9  
 A:Note: KIAA1062  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.4%; Score 8; DB 2; Length 1529;  
 Best local similarity 100.0%; Pred. No. 42;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 11111111  
 Db 133 GLEPPTSG 140

## RESULT 13

S71363  
 Probable ATP-binding cassette transporter ABC-3 - human  
 N:Alternate names: ATP-binding cassette transporter ABC-C  
 C:Species: Homo sapiens (man)  
 C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 02-Feb-2001  
 C:Accession: S71363  
 R:Krupbauer, N.; Hofmann, F.  
 FEBS Lett. 391, 61-65, 1996  
 A:Title: Primary structure of a novel ABC transporter with a chromosomal localization of  
 A:Reference number: S71363; MIM:9632608; PMID:8706931  
 A:Accession: S71363  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1704 <K1U>  
 A:Cross-references: EMBL:X97187; NID:q1514529; PIDN:CA65825.1; PID:e243436; PID:q151453  
 A:Experimental source: cell line medullary thyroid carcinoma  
 C:Genetics:  
 A:Gene: GDB:ABC3  
 A:Cross-references: GDB:3770735; OMIM:601615  
 A:Map position: 16p13.3-16p13.3  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
 C:Keywords: ATP binding; nucleotide binding; P-loop; phosphoprotein; transmembrane prote  
 F:253-283/Domain: transmembrane #status predicted <TM1>  
 F:307-329/Domain: transmembrane #status predicted <TM2>  
 F:345-364/Domain: transmembrane #status predicted <TM3>  
 F:373-394/Domain: transmembrane #status predicted <TM4>  
 F:401-422/Domain: transmembrane #status predicted <TM5>  
 F:432-475/Domain: transmembrane #status predicted <TM6>  
 F:549-739/Domain: ATP-binding cassette homology <ABC>  
 F:566-573/Region: nucleotide-binding motif A (P-loop)  
 F:685-690/Region: nucleotide-binding motif B  
 F:1100-1120/Domain: transmembrane #status predicted <TM7>  
 F:1145-1169/Domain: transmembrane #status predicted <TM8>  
 F:1181-1207/Domain: transmembrane #status predicted <TM9>  
 F:1215-1236/Domain: transmembrane #status predicted <TM10>  
 F:1245-1264/Domain: transmembrane #status predicted <TM11>

F:1299-1324/Domain: transmembrane #status predicted <TM12>  
 F:1399-1590/Domain: ATP-binding cassette homology <ABC2>  
 F:1416-1423/Region: nucleotide-binding motif A (P-loop)  
 F:1535-1540/Region: nucleotide-binding motif B  
 F:674, 866, 1524/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #  
 F:1344/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status p

Query Match 1.4%; Score 8; DB 2; Length 1704;  
 Best local similarity 100.0%; Pred. No. 46;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 11111111  
 Db 581 GLEPPTSG 588

## RESULT 14

A59188  
 ATP-binding cassette transporter ABC3 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 17-May-2002  
 C:Accession: A59188  
 R:Connors, T.D.; Van Raay, T.J.; Petry, L.R.; Klinger, K.W.; Landes, G.M.; Burn, T.C  
 Genomics 39, 231-234, 1997  
 A:Title: The cloning of a human ABC gene (ABC3) mapping to chromosome 16p13.3.  
 A:Reference number: A59188; MIM:97179225; PMID:9027511  
 A:Accession: A59188  
 A:Status: preliminary: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1704 <CON>  
 A:Cross-references: GB:U78735; NID:q1699037; PIDN:AC50967.1; PID:q1699038  
 C:Genetics:  
 A:Gene: GDB:ABC3  
 A:Cross-references: GDB:3770735; OMIM:601615  
 A:Map position: 16p13.3-16p13.3  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.4%; Score 8; DB 2; Length 1704;  
 Best local similarity 100.0%; Pred. No. 46;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 11111111  
 Db 581 GLEPPTSG 588

## RESULT 15

A54774  
 ATP binding cassette transporter ABC1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Apr-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Feb-2001  
 C:Accession: A54774  
 R:Uchiani, M.F.; Demizot, F.; Savary, S.; Mattei, M.G.; Chimal, G.  
 Genomics 21, 150-159, 1994  
 A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.  
 A:Reference number: A54774; MIM:94375008; PMID:8068782  
 A:Accession: A54774  
 A:Molecule type: mRNA  
 A:Residues: 1-2201 <KUC>  
 A:Cross-references: GB:X75926; NID:q495256; PIDN:CA53530.1; PID:q495257  
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
 C:Keywords: ATP; duplication; nucleotide binding; P-loop  
 F:856-1047/Domain: ATP-binding cassette homology <ABC1>  
 F:873-880/Region: nucleotide-binding motif A (P-loop)  
 F:1869-2060/Domain: ATP-binding cassette homology <ABC2>  
 F:1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 1.4%; Score 8; DB 2; Length 2201;  
 Best local similarity 100.0%; Pred. No. 58;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPTSG 381  
 11111111

Thu Apr 17 07:55:17 2003

us-09-897-778-176.Oligo.rpr

Page 5

Db 888 GLEPPNSG 895

Search completed: April 16, 2003, 16:37:37  
Job time : 56.0788 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:23:10 ; Search time 29.4729 Seconds  
(without alignments)  
814.809 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 579  
Sequence: 1 MNKLYGNLSNAPSDLES.....VKHQOQKALQSGPPQSRK 579

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Swissprot\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.4	84	1 YCX9_OENHO	Q9m6m6 oenothera h
2	8	1.4	311	1 RBFL_MOUSE	P22560 mus musculu
3	8	1.4	997	1 BIRL_SCHPO	O14064 schizosacch
4	8	1.4	1000	1 Y083_CAEEL	P34619 caenorhabdi
5	8	1.4	1704	1 ABC3_HUMAN	O99758 homo sapien
6	8	1.4	2261	1 ABC1_HUMAN	O95477 homo sapien
7	8	1.4	2261	1 ABC1_MOUSE	P41333 mus musculu
8	8	1.4	2434	1 ABC2_HUMAN	P41234 mus musculu
9	8	1.4	2434	1 ABC2_MOUSE	O9b2c7 homo sapien
10	8	1.4	3164	1 TEGU_HSV11	P10220 herpes simp
11	8	1.2	146	1 RL15_BACSU	P19946 bacillus su
12	7	1.2	153	1 HS11_SOYBN	P02519 glycine max
13	7	1.2	183	1 YUGA_ECOLI	P26550 escherichia
14	7	1.2	203	1 CIT1_MOUSE	P97769 mus musculu
15	7	1.2	232	1 YY26_MYCTU	Q50702 mycobacteri
16	7	1.2	239	1 FLA3_METVO	P27805 methanococc
17	7	1.2	285	1 YK62_CAEEL	P45528 caenorhabdi
18	7	1.2	286	1 YRAL_ECOLI	P45528 escherichia
19	7	1.2	291	1 ERA_CAMJE	O9ph11 campylobact
20	7	1.2	299	1 ERA_STAM	O99f59 staphylococ
21	7	1.2	301	1 ERA_AOUAE	O67800 aquifex aeo
22	7	1.2	301	1 ERA_LISMO	O92dp8 listeria in
23	7	1.2	301	1 ERA_LISMO	O8y750 listeria mo
24	7	1.2	302	1 RS3_HALNI	P15009 halobacteri
25	7	1.2	304	1 RS3_HALMA	P20281 haloarcula
26	7	1.2	310	1 YIHG_ECOLI	P32129 escherichia
27	7	1.2	311	1 TUS_YERPE	O916x9 yeastina pe
28	7	1.2	330	1 PDXA_XYLFA	O9p139 xyella fas
29	7	1.2	333	1 TRPD_HAENI	P43858 haemophilus
30	7	1.2	346	1 TERC_ALCSP	P18780 alcaligenes
31	7	1.2	352	1 TERC_SERMA	O52356 serratia ma
32	7	1.2	352	1 RFL_HELPY	P55998 helicobacte
33	7	1.2	355	1 AMPN_ACEPA	O10736 acetobacter

34	7	1.2	359	1 AROC_CHLUPN	Q926m2 chlamydia p
35	7	1.2	367	1 Y001_CAEEL	Q09293 caenorhabdi
36	7	1.2	389	1 NDOP_MOUSE	Q03173 mus musculu
37	7	1.2	399	1 EFTU_PRRIS	O50340 fervidobact
38	7	1.2	431	1 TIG_XYLFA	O9p42 xyella fas
39	7	1.2	449	1 YMG5_CAEEL	O20932 caenorhabdi
40	7	1.2	463	1 ROK_HUMAN	O07244 homo sapien
41	7	1.2	463	1 ROK_RABIT	O19049 oryctolagus
42	7	1.2	464	1 OTSA_RHISN	P55612 rhizobium s
43	7	1.2	464	1 ROK_MOUSE	O60577 mus musculu
44	7	1.2	484	1 FKHL_YEAST	P40466 saccharomyc
45	7	1.2	486	1 CDSN_HUMAN	O15517 homo sapien

## ALIGNMENTS

RESULT 1	
YCX9_OENHO	STANDARD: PRT: 84 AA.
ID YCX9_OENHO	
AC Q9m6m6:	
DT 15-JUN-2002 (Rel. 41, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last sequence update)	
DE Hypothetical 9.7 kDa protein in trnC-rpoB intergenic region (ORF84).	
OS Oenothera hookeri (Hooker's evening primrose).	
OC Chloroplast.	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC eucosids II; Myrtales; Onagraceae; Oenothera.	
OX NCBI_TaxID=85636;	
ON [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Johansen;	
RK MEDLINE-20309318; PubMed-10852478;	
RA Hupfer H., Swatek M., Hornung S., Herrmann R.G., Water R.M.,	
RA Chiu W.-L., Sears B.;	
RT "Complete nucleotide sequence of the Oenothera elata plastid	
RT chromosome, representing plastome I of the five distinguishable	
RT Euenothera plastomes.";	
RT Mol. Gen. Genet. 263:581-585(2000).	
CC -----	
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CC -----	
DR EMBL: AJ271079; CAB67150.1; "	
KW Chloroplast; Hypothetical protein.	
SO SEQUENCE 84 AA; 9674 MW; D37B6A918546E0CB CRC64;	
Query Match	1.4%; Score 8; DB 1; Length 84;
Best Local Similarity	100.0%; Pred. No. 1.4;
Matches 8; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY 358 MNLOAHLI 365	
DB 1 MNLOAHLI 8	
RESULT 2	
RBFL_MOUSE	STANDARD: PRT: 311 AA.
ID RBFL_MOUSE	
AC P22560:	
DT 01-AUG-1991 (Rel. 19, Created)	
DT 01-AUG-1991 (Rel. 19, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE IFN-response binding factor 1 (IRBF-1).	
GN IREBFL.	
OS Mus musculus (Mouse).	

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss albino;
RX MEDLINE=91095416; Pubmed=1986360;
RA "van C., Tamm I.;"
RT "Molecular cloning and characterization of interferon alpha/beta
RT response element binding factors of the murine (2'-5')oligoadenylate
RT synthetase ME-12 gene.;"
RL Proc. Natl. Acad. Sci. U.S.A. 88:144-148(1991).
CC -1- FUNCTION: BINDS INTERFERON RESPONSE ELEMENTS (IRE).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
CC -----
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CC -----
DR EMBL: M55290; AAA37884.1; -
DR FIR: A38558; A38558.
DR TRANSFAC: T00421; -
DR MGD: MGI:1930074; Irbefl.
KW Phosphorylation; Transcription regulation; DNA-binding;
KW Nuclear protein.
FT SIMILAR 46 83 TO GAL4 DNA-BINDING DOMAIN.
FT DOMAIN 161 184 ASP/GLU-RICH (ACIDIC).
FT MOD_RES 256 270 LEUCINE-ZIPPER.
FT MOD_RES 90 90 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 247 247 PHOSPHORYLATION (BY CK2) (POTENTIAL).
SQ SEQUENCE 311 AA; 35564 MW; AC45C725162EB03 CRC64;

Query Match 1.4%; Score 8; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NKLXGNL 9
Db 106 NKLXGNL 113

RESULT 3
BIRL SCHPO STANDARD; PRT; 997 AA.
AC 014064;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE BIR1 protein (Chromosome segregation protein cul17).
DE BIR1 OR CUL17 OR PHR1 OR SPC92.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC NCBI_TaxId=4896;
RX MEDLINE=21439264; Pubmed=11554922;
RA Morishita J., Matsusaka T., Goshima G., Nakamura T., Tatebe H.,
RA Yanagishita M.;
RT "BIR1/cul17 moving from chromosome to spindle upon the loss of
RT cohesion is required for condensation, spindle elongation and
RT repair.;"
RL Genes Cells 6:743-763(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; Pubmed=11859360;

```

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellgett J., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson S., Saunders D., Seeger S., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymopiez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moeschel D., Hübner H.,
RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandt R., Punnett B.,
RA Gallbrecht A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.K., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen O., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe.;"
RA Nature 415:871-880(2002).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=99398681; Pubmed=10468581;
RA Uren A.G., Bellharz T., O'Connell M.J., Bugg S.J., van Driel R.,
RA Vaux D.L., Lithgow T.;
RT "Role for yeast inhibitor of apoptosis (IAP)-like proteins in cell
RT division.;"
RL Proc. Natl. Acad. Sci. U.S.A. 96:10170-10175(1999).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=21850422; Pubmed=11861551;
RA Rajagopalan S., Balasubramanian M.K.;
RT "Schizosaccharomyces pombe BIR1p, a nuclear protein that localizes to
RT kinetochores and the spindle midzone, is essential for chromosome
RT condensation and spindle elongation during mitosis.;"
RL Genetics 160:445-456(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=20035862; Pubmed=10571085;
RA Rajagopalan S., Balasubramanian M.K.;
RT "S. pombe Pph1p, an inhibitor of apoptosis domain containing protein,
RT is essential for chromosome segregation.;"
RL FEBS Lett. 460:187-190(1999).
CC -1- FUNCTION: Seems to act in the pleiotropic control of cell
CC division. Has a role in chromosome segregation by recruiting
CC condensin and atkl kinase to appropriate sites as the cell
CC progresses through mitosis.
CC -1- SUBCELLULAR LOCATION: Nuclear. Interacts with the outer
CC centromeric regions of the chromosomes during interphase. After
CC chromatin separates moves to the middle of the spindle.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -----
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CC -----
DR EMBL: AB031034; BA883415.1; -
DR HSSP: A1031323; CAA20434.1; -
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR. 2.
DR SMART: SM00238; BIR. 2.
DR PROSITE: PS01282; BIR_REPEAT_1; FALSE_NEG.

```

DR PROSITE: PS50143; BIR\_REPEAT\_2; 2.  
 KW Cell division; Mitosis; Nuclear protein; Repeat.

FT REPEAT 25 99 BIR 1.  
 FT REPEAT 120 194 BIR 2.  
 FT DOMAIN 80 83 POLY-ASP.  
 FT DOMAIN 312 319 POLY-ASP.  
 FT DOMAIN 487 490 POLY-SER.  
 SQ SEQUENCE 997 AA; 112579 MW; 952A6BAF5A489F4 CRC64;

Query Match 1.4%; Score 8; DB 1; Length 997;  
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 FTEETPLK 280  
 111111111  
 DB 342 FTEETPLK 349

## RESULT 4

Y083 CAEEL STANDARD; PRT; 1000 AA.  
 AC P34619;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical 113.4 Kda protein ZK1236.3 in chromosome III.  
 GN ZK1236.3  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94130718; PubMed=7906398;  
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Gratton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
 RA Sims M., Smailson N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Sulston J., Thierrey-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 RA Wohlschlag P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RL Nature 368:32-38(1994).  
 CC -----

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 CC -----

CC EMBL: L13200; AAA28193.1; -  
 DR PIR: S44898; S44898.  
 DR Wormpep: ZK1236.3; CE00532.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1000 AA; 113419 MW; D230C9A6F84928E2 CRC64;

Query Match 1.4%; Score 8; DB 1; Length 1000;  
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 PSDLESIF 22  
 111111111  
 DB 568 PSDLESIF 575

## RESULT 5

ABC3\_HUMAN STANDARD; PRT; 1704 AA.  
 ID ABC3\_HUMAN  
 AC Q99758; Q92473;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ATP-binding cassette, sub-family A, member 3 (ATP-binding cassette  
 DE transporter 3) (ATP-binding cassette 3) (ABC-C transporter).  
 GN ABC3 OR ABC3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thyroid carcinoma;  
 RX MEDLINE=96326608; PubMed=8706931;  
 RA Klugbauer N., Hofmann F.;  
 RT "Primary structure of a novel ABC transporter with a chromosomal  
 RT localization on the band encoding the multidrug resistance-associated  
 RT protein.";  
 RL FEBS Lett. 391:61-65(1996).  
 RN 121  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179225; PubMed=9027511;  
 RA Connors T.D., van Raay T.J., Petry L.R., Klinger K.W., Landes G.M.,  
 RA Burn T.C.;  
 RT "The cloning of a human ABC gene (ABC3) mapping to chromosome  
 RT 16p13.3.";  
 RL Genomics 39:231-234(1997).  
 CC -----

CC -1- FUNCTION: MAY BE A TRANSPORTER. ITS NATURAL SUBSTRATE HAS NOT BEEN  
 CC FOUND YET (BY SIMILARITY). MAY ACT AS AN EFFLUX PUMP FOR  
 CC CHEMOTHERAPEUTIC DRUGS.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, FOLLOWED BY BRAIN,  
 CC PANCREAS, SKELETAL MUSCLE AND HEART. WEAKLY EXPRESSED IN PLACENTA,  
 CC KIDNEY AND LIVER. ALSO EXPRESSED IN MEDULLARY THYROID CARCINOMA  
 CC CELLS (MTC) AND IN C-CELL CARCINOMA.  
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
 CC ATP BINDING CASSETTE (ABC) DOMAIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY, ABCA SUBFAMILY.  
 CC -----

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 CC -----

CC EMBL: U78735; AAC50967.1; -  
 DR EMBL: X97187; CAAC5825.1; -  
 DR Genew; HGNC:33; ABCA3.  
 DR MIM; 601615; -  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_transportr.  
 DR Pfam: PF00005; ABC\_tran; 2.  
 DR Prodom: PD000006; ABC\_transportr; 2.  
 DR SMART: SMO0382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER; 1.  
 KW ATP-binding; Transport; Transmembrane.  
 SQ SEQUENCE 1704 AA; 1704 MW; 1183 TRANSMEM  
 FT TRANSMEM 22 42  
 FT TRANSMEM 249 269  
 FT TRANSMEM 307 327  
 FT TRANSMEM 344 364  
 FT TRANSMEM 373 393  
 FT TRANSMEM 405 425  
 FT TRANSMEM 447 467  
 FT TRANSMEM 495 515  
 FT TRANSMEM 547 567  
 FT TRANSMEM 599 619  
 FT TRANSMEM 651 671  
 FT TRANSMEM 703 723  
 FT TRANSMEM 755 775  
 FT TRANSMEM 807 827  
 FT TRANSMEM 859 879  
 FT TRANSMEM 911 931  
 FT TRANSMEM 963 983  
 FT TRANSMEM 1015 1035  
 FT TRANSMEM 1067 1087  
 FT TRANSMEM 1119 1139  
 FT TRANSMEM 1171 1191  
 FT TRANSMEM 1223 1243  
 FT TRANSMEM 1295 1315  
 FT TRANSMEM 1367 1387  
 FT TRANSMEM 1419 1439  
 FT TRANSMEM 1491 1511  
 FT TRANSMEM 1543 1563  
 FT TRANSMEM 1615 1635  
 FT TRANSMEM 1687 1703  
 FT TRANSMEM 1703 1703

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FT TRANSMEM 1213 1233 POTENTIAL.
FT TRANSMEM 1245 1265 POTENTIAL.
FT TRANSMEM 1306 1326 POTENTIAL.
FT NP_BIND 566 573 ATP (POTENTIAL).
FT NP_BIND 1416 1423 ATP (POTENTIAL).
FT CONFLICT 36 36 P -> S (IN REF. 2).
FT CONFLICT 196 196 L -> P (IN REF. 2).
SO SEQUENCE 1704 AA; 191387 MW; AF0098DAFA7A04F5F CRC64;

Query Match 1.4%; Score 8; DB 1; Length 1704;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GLEPPPSG 381
DB 581 GLEPPPSG 588

RESULT 6
ABCI_HUMAN STANDARD; PRT: 2261 AA.
ID ABC1_HUMAN
AC 095477; Q9UN08; Q9UN07; Q9UN06; Q9UN04; Q9UN09; Q96T85; Q96S56;
DT 16-OCT-2001 (rel. 40; Created)
DT 16-OCT-2001 (rel. 40; Last annotation update)
DT 15-JUN-2002 (rel. 41; Last annotation update)
DE ABC1-binding cassette, sub-family A, member 1 (ATP-binding cassette
transporter 1) (ATP-binding cassette 1) (ABC-1) (cholesterol efflux
transporter 1) (protein).
NC ABC1 OR ABC OR ABCP.
CC Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE-20345099; PubMed-10884428;
RA Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qiu Y.,
RA Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,
RA Handen-Schlid C.C., Prades C., Chimini G., Blackman E.E.,
RA Francois T.L., Duverger N., Rubin E.M., Rosier M., Deneffe P.,
RA Fredrickson D.S., Brewer H.B. Jr.;
RT "Complete genomic sequence of the human ABCA1 gene: analysis of the
human and mouse ATP-binding cassette A promoter."
RL Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).
RN 121
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Schwartz K., Lawn R.M., Wade D.P.;
RT "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RX MEDLINE-21251004; PubMed-11352567;
RA Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT "Human and mouse ABCA1 comparative sequencing and chengesis
studies revealing novel regulatory sequences."
RL Genomics 73:66-76(2001).
RN 141
RP SEQUENCE FROM N.A.
RA Tanaka A.R., Abe-Domae S., Arikawa R., Sadanami K., Kidera A.,
RA Kikita N., Amachi T., Yokoyama S., Ueda K.;
RT "A new topological model of functional human ABCA1-signal peptide
cleavage and glycosylation of a large extracellular domain."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 151
RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE-99194549; PubMed-10092505;
RA Langmann T., Klucken T., Reil M., Liebisch G., Luciani M.F.,
RA Chamlani G., Kaminski W.E., Schmitz G.;
RT "Molecular cloning of the human ATP-binding cassette transporter 1
(ABCA1): evidence for sterol-dependent regulation in macrophages."
RL Biochem. Biophys. Res. Commun. 257:29-33(1999).

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RN 161
RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE-99364413; PubMed-10431238;
RA Rust S., Rosier M., Funke H., Real J., Amour Z., Piette J.-C.,
RA Deluize J.-F., Brewer H.B., Duverger N., Deneffe P., Assmann G.;
RT "Tangier disease is caused by mutations in the gene encoding
ATP-binding cassette transporter 1."
RN Nat. Genet. 22:352-355(1999).
RN 171
RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.
RX MEDLINE-20001430; PubMed-10533863;
RA Marcell M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,
RA Collins J.A., Van Dam M., Molhuizen H.O.F., Loubser O.,
RA Boucheir B., Pimstone S., Fichter K., Mott S., Denis M.,
RT "Mutations in the ABC1 gene in familial HDL deficiency with defective
cholesterol efflux."
RL Lancet 354:1341-1346(1999).
RN 181
RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.
RX MEDLINE-99364411; PubMed-10431236;
RA Brooks-Wilson A., Marcell M., Clee S.M., Zhang L.-H., Roomp K.,
RA Van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
RA Lousser O., Ouellette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
RA Sengen C.W., Scherer S., Mott S., Denis M., Martindale D.,
RA Broholm K., Koop B., Pimstone S., Kastelein J.J.P.,
RA Hayden M.R.;
RT "Mutations in ABC1 in Tangier disease and familial high-density
lipoprotein deficiency."
RN Nat. Genet. 22:336-345(1999).
RN 191
RP VARIANTS TD SER-590, SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
MET-883.
RX MEDLINE-99364412; PubMed-10431237;
RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
RA Diederich W., Drobnik W., Barlag S., Buehler C.,
RA Porch G., Oesteruermer M., Kaminski W.E., Hahmann H.W., Oette K.,
RA Rothe G., Asanidis C., Lackner K.J., Schmitz G.;
RT "The gene encoding ATP-binding cassette transporter 1 is mutated in
Tangier disease."
RN Nat. Genet. 22:347-351(1999).
RN 1101
RP VARIANTS TD ILE-929; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693
DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
RX MEDLINE-20540002; PubMed-11086027;
RA Clee S.M., Kastelein J.J.P., Van Dam M., Marcell M., Roomp K.,
RA Zwarts K.Y., Collins J.A., Roelants R., Tamasawa N., Stulic T.,
RA Suda T., Ceska R., Boucher B., Rondeau G., Desoulh C.,
RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
RA Hayden M.R.;
RT "Age and residual cholesterol efflux affect HDL cholesterol levels and
coronary artery disease in ABCA1 heterozygotes."
RL J. Clin. Invest. 106:1263-1270(2000).
RN 1111
RP VARIANTS TD ASN-1289 AND HIS-1800.
RX MEDLINE-20171564; PubMed-10706591;
RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
RA Van Eerdewegh P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,
RA Vasek-Mckenna D., O'Neill G., Eberhart G.P., Wellfienbach B.,
RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;
RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four
Tangier disease kindreds."
RL J. Lipid Res. 41:433-441(2000).
RN 1121
RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;
ILE-825; MET-883 AND LYS-1587.
RX MEDLINE-20396633; PubMed-10938023;
RA Wang J., Burnett J.R., Near S., Young K., Zimman B., Hanley A.J.G.,
RA Connolly P.W., Harris S.B., Hegele R.A.;
RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol."
RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
RN 1131
RP VARIANT TD TRP-587, AND VARIANT LEU-2168.

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CC MEDLINE=21157002; PubMed=11257260;  
 RA Bertolini S., Pisciotto L., Seri M., Cusano R., Cantafora A.,  
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;  
 RT "A point mutation in ABCI gene in a patient with severe premature  
 RT coronary heart disease and mild clinical phenotype of Tangier  
 RT disease.";  
 RL Atherosclerosis 154:599-605(2001).  
 RN [14]  
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.  
 RX MEDLINE=21157003; PubMed=11257261;  
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kielar D.,  
 RA Probst M., Ordovas J.M., Aslanidis C., Lackner K.J.,  
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,  
 RA Schmitz G.;  
 RT "Common variants in the gene encoding ATP-binding cassette transporter  
 RT 1 in men with low HDL cholesterol levels and coronary heart disease.";  
 RL Atherosclerosis 154:607-611(2001).  
 RN [15]  
 RP VARIANT TD LEU-1506.  
 RX MEDLINE=21369429; PubMed=11476961;  
 RA Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kielar D., Probst M.,  
 RA Kiec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,  
 RA Sutrop N., Schmitz G.;  
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of  
 RT the ABCA1 gene and its application in genetic analysis of a new  
 RT patient with familial high-density lipoprotein deficiency syndrome.";  
 RL Biochim. Biophys. Acta 1537:42-48(2001).  
 RN [16]  
 RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.  
 RX MEDLINE=21369433; PubMed=11476965;  
 RA Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,  
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;  
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier  
 RT disease and familial high density lipoprotein deficiency with  
 RT coronary heart disease.";  
 RL Biochim. Biophys. Acta 1537:71-78(2001).  
 RN [17]  
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;  
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.  
 RX MEDLINE=21138379; PubMed=11238261;  
 RA Clee S.M., Zwiderman A.H., Engert J.C., Zwarts K.Y.,  
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Miland M., van Dam M.,  
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,  
 RA Hayden M.R.;  
 RT "Common genetic variation in ABCA1 is associated with altered  
 RT lipoprotein levels and a modified risk for coronary artery disease.";  
 RL Circulation 103:1198-1205(2001).  
 RN [18]  
 RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.  
 RX MEDLINE=21645894; PubMed=11785958;  
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,  
 RA Ishihara M., Sakane N., Zhang Z., Tsuji K., Matsuyama A., Ohama T.,  
 RA Matsura F., Ishigami M., Sakai N., Hirooka H., Hattori H.,  
 RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,  
 RA Yanahita S., Matsuzawa Y.;  
 RT "Expression and functional analyses of novel mutations of ATP-binding  
 RT cassette transporter-1 in Japanese patients with high-density  
 RT lipoprotein deficiency.";  
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).  
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION  
 CC TRANSPORT. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL  
 CC TRANSPORT.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN  
 CC MACROPHAGES.  
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
 CC ATP BINDING CASSETTE (ABC) DOMAIN.  
 CC -1- DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN  
 CC DEFICIENCY TYPE I (HDLI). ALSO KNOWN AS TANGIER DISEASE (TD). TD  
 CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY  
 CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,  
 CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY  
 CC DISEASE (CAD).

CC -1- DISEASE: Defects in ABCA1 are a cause of high density lipoprotein  
 Query Match 1.4%; Score 8; DB 1; Length 2261;  
 Best local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 374 GLEPPTSG 381  
 DB 948 GLEPPTSG 955  
 RESULT 7  
 ID ABCI MOUSE STANDARD; PRT; 2261 AA.  
 AC P41233;  
 DT 01-FEB-1995 (rel. 31, Created)  
 DT 16-OCT-2001 (rel. 40, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette  
 DE transporter 1) (ATP-binding cassette 1) (ABC-1).  
 GN ABCA1 OR ABCI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DKA/2; TISSUE=Macrophage;  
 RA MEDLINE=94375008; PubMed=8088782;  
 RT Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;  
 RT "Cloning of two novel ABC transporters mapping on human chromosome  
 RT 9.";  
 RL Genomics 21:150-159(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C37BL/6J;  
 RA Qiu Y., Cavelier L., Chiu S., Rubin E., Cheng J.-F.;  
 RT "Human and mouse ABCA1 comparative sequencing and transgenesis studies  
 RT identify potential regulatory sequences.";  
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION  
 CC TRANSPORT. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL  
 CC TRANSPORT (BY SIMILARITY)  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST  
 CC LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.  
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
 CC ATP BINDING CASSETTE (ABC) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X75926; CAA53530.1; ALT\_INIT.  
 DR EMBL: AF287263; AAG39073.1; ALT\_INIT.  
 DR MGD: MG1:96607; ABCA1.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_Transport.  
 DR Pfam: PF00005; ABC\_tran; 2.  
 DR ProDom: PD000006; ABC\_Transport; 2.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_Transporter; 1.  
 KM APP-binding: Glycoprotein; Transmembrane; Transport.  
 FT TRANSMEM 26 42  
 FT TRANSMEM 640 656 POTENTIAL.  
 FT TRANSMEM 690 706 POTENTIAL.  
 FT TRANSMEM 717 733 POTENTIAL.  
 FT TRANSMEM 749 765 POTENTIAL.

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FT TRANSMEM 771 787 POTENTIAL.
FT TRANSMEM 1041 1057 POTENTIAL.
FT TRANSMEM 1351 1367 POTENTIAL.
FT TRANSMEM 1661 1677 POTENTIAL.
FT TRANSMEM 1708 1724 POTENTIAL.
FT TRANSMEM 1737 1753 POTENTIAL.
FT TRANSMEM 1775 1791 POTENTIAL.
FT TRANSMEM 1854 1870 POTENTIAL.
FT NP_BIND 933 940 ATP (POTENTIAL).
FT NP_BIND 1946 1953 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 820 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1144 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1294 1294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1453 1453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1504 1504 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1637 1637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2044 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2238 2238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1567 1568 MISSING (IN REF. 2).
FT CONFLICT 2024 2024 MISSING (IN REF. 2).
SQ SEQUENCE 2261 AA: 254011 MW: 546252.1PDI0999 CRC64:

Query Match 1.4%; Score 8; DB 1; Length 2261;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 374 GLEPPTSG 381
Db 948 GLEPPTSG 955

RESULT 8
ABC2_MOUSE STANDARD: PRT: 2434 AA.
ID ABC2_MOUSE
AC P41234;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 2 (ATP-binding cassette transporter 2) (ATP-binding cassette 2).
GN ABCA2 OR ABC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND REVISIONS.
RC STRAIN-DBA/2;
RA Chimini G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBD databases.
RN [2]
RP SEQUENCE OF 964-2434 FROM N.A.
RC STRAIN-DBA/2; TISSUE=Macrophage;
RX MEDLINE=94375008; PubMed=8088782;
RA Luciani M.F., Dentzov F., Savary S., Mattei M.-G., Chimini G.;
RT Cloning of two novel ABC transporters mapping on human chromosome 9.
RT Genomics 21:150-159(1994).
-!- FUNCTION: PROBABLE TRANSPORTER, ITS NATURAL SUBSTRATE HAS NOT BEEN

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CC CC FOUND YET. MAY HAVE A ROLE IN MACROPHAGE LIPID METABOLISM AND
CC CC NEURAL DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC LEVELS ARE FOUND IN BRAIN AND PREGNANT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
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CC -----
DR EMBL: X75927; CAA3531.2; -.
DR MGI: 99606; Abca2.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00005; ABC_tran. 2.
DR ProDom: PD000006; ABC_transporter. 2.
DR SMART: SM00382; AAA. 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Transport; Transmembrane; Repeat; Glycoprotein.
KW TRANSMEM 21
FT TRANSMEM 705 727 POTENTIAL.
FT TRANSMEM 748 770 POTENTIAL.
FT TRANSMEM 780 802 POTENTIAL.
FT TRANSMEM 809 831 POTENTIAL.
FT TRANSMEM 1793 1815 POTENTIAL.
FT TRANSMEM 1846 1865 POTENTIAL.
FT TRANSMEM 1875 1897 POTENTIAL.
FT TRANSMEM 1904 1926 POTENTIAL.
FT NP_BIND 1024 1031 ATP (POTENTIAL).
FT NP_BIND 2088 2095 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 589 589 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 599 599 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1408 1408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1466 1466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1549 1549 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1557 1557 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1776 1776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2055 2055 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2434 AA: 270582 MW: 348948.5692005 CRC64:

Query Match 1.4%; Score 8; DB 1; Length 2434;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 374 GLEPPTSG 381
Db 1039 GLEPPTSG 1046

RESULT 9
ABC2_HUMAN

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DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE Large tegument protein (Virion protein UL36).  
 GN UL36.  
 OS Herpes simplex virus (type 1 / strain 17).  
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 NX NCBI\_TaxID=10299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=86274327; PubMed=2839584;  
 RA McGeech D.J., Daillymple M.A., Davison A.J., Dolan A., Frame M.C.,  
 RA McNab D., Perry L.J., Scott J.E., Taylor P.;  
 RT The complete DNA sequence of the long unique region in the genome of  
 RT Herpes simplex virus type 1.;  
 RT J. Gen. Virol. 69:1531-1574(1988).  
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,  
 CC EHV-1 24, BBV BP1FL1, HVS-1 64, VZV 22, AND HCMV UL48.  
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 CC -----  
 DR EMBL: X14112; CAA32311.1;  
 DR PIR: I30085; WHEHE6.  
 DR InterPro: IPR005210; Herpes\_UL36.  
 DR Pfam: PF03586; Herpes\_UL36; 1.  
 KM Repeat.  
 FT 2911 2960 35 X 2 AA TANDEM REPEATS OF P-Q.  
 SO DOMAIN  
 SEQUENCE 3164 AA; 335857 MW; CC5D31FF4F9FE3FA CRC64;  
 QY 383 PPPTSGPP 390  
 DB 2857 PPPTSGPP 2864  
 Query Match 1.4%; Score 8; DB 1; Length 3164;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 2857 PPPTSGPP 2864  
 RESULT 11  
 ID RL15\_BACSU STANDARD; PRT; 146 AA.  
 AC P19946;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein L15.  
 GN RPL0.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90292990; PubMed=2113521;  
 RA Nakamura K., Nakamura A., Takematsu H., Yoshikawa H., Yamane K.;  
 RT Cloning and characterization of a Bacillus subtilis gene homologous  
 RT to E. coli secY.;  
 RT J. Biochem. 107:603-607(1990).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 RA MEDLINE=90221911; PubMed=2139212;  
 RA Yoshikawa H., Doi R.H.;  
 RT "Sequence of the Bacillus subtilis spectinomycin resistance gene  
 RT region";  
 RU Nucleic Acids Res. 18:1647-1647(1990).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / Marburg;  
 RX MEDLINE=96166897; PubMed=8635744;  
 RT Sun J.-W., Boylan S.A., Oh S.H., Price C.W.;  
 RT Genetic and transcriptional organization of the Bacillus subtilis  
 RT spe-alpha region.;  
 RT Gene 169:17-23(1996).  
 RN [4]  
 RP SEQUENCE OF 94-146 FROM N.A.  
 RC STRAIN-168;  
 RX MEDLINE=90251170; PubMed=2110998;  
 RA Suh J.-W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,  
 RA Price C.W.;  
 RT "Isolation of a secY homologue from Bacillus subtilis: evidence for a  
 RT common protein export pathway in eubacteria";  
 RT Mol. Microbiol. 4:305-314(1990).  
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL: D00619; BAA00494.1;  
 DR EMBL: X51329; CAA35711.1;  
 DR EMBL: L47971; AAB06818.1;  
 DR EMBL: M31102; AAB59117.1;  
 DR EMBL: Z99104; CAB11911.1;  
 DR PIR: S12682; RSBSU5.  
 DR Subtilist; BG10444; RPL0.  
 DR InterPro: IPR001196; Ribosomal\_L15.  
 DR Pfam: PF00256; L15; 1.  
 DR Pfam: PF01305; Ribosomal\_L15; 1.  
 DR TIGRfams: TIGR01071; rpl0\_bact; 1.  
 DR PROSITE: PS00475; RIBOSOMAL\_L15; 1.  
 KW Ribosomal protein; rRNA-binding; Complete proteome.  
 SO SEQUENCE 146 AA; 15383 MW; 5DB07A902B26C11 CRC64;  
 QY 136 LDKLNGF 142  
 DB 79 LDKLNGF 85  
 Query Match 1.2%; Score 7; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 79 LDKLNGF 85  
 RESULT 12  
 ID HS11\_SOYBN STANDARD; PRT; 153 AA.  
 AC P02519;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE 17.3 kDa class I heat shock protein (HSP 17.3).  
 GN HSP17.3-B OR H86871.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 NX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schorff F., Raschke E., Nagao R.T.;  
 RT "The DNA sequence analysis of soybean heat-shock genes and  
 RT identification of possible regulatory promoter elements";  
 RL EMO J. 3:2491-2497(1984).  
 CC -1- SUBUNIT: FORMS OLIGOMERIC STRUCTURES.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

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CC -1- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
CC FAMILY:
CC -1- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
CC WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
CC AND CLASS IV WHICH IS IN THE ENOMEMBRANE. THIS PROTEIN BELONGS
CC TO CLASS I.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: X01104; CAA25578.1; -
CC PIR: A02922; HHSY17.
CC InterPro: IPR002068; Hsp20.
CC Pfam: PF00011; HSP20; 1.
CC PROSITE: PS01031; HSP20; 1.
CC Heat shock; Multigene family.
CC KW
CC SEQUENCE 153 AA; 17347 MW; A1A8612B9EC86819 CRC64;
SQ
Query Match 1.2%; Score 7; DB 1; Length 153;
Best local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 483 KEEVKLE 489
| | | | |
Db 68 KEEVKLE 74
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RESULT 13
YCGA_ECOLI STANDARD: PRT; 183 AA.
ID YCGA_ECOLI
AC P26650;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yj9A (y96 protein).
GN YCGA OR X96 OR B4234 OR Z5844 OR ECS5211.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RA Rodriguez-Sainz M.C., Moreno F.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=96177756; PubMed=8604133;
RA Moriyama N., Shimizu H., Takiguchi S., Baba Y., Amino H.,
RA Horinouchi T., Sekimizu K., Miki T.;
RT "Evidence for involvement of Escherichia coli genes pmhA, csrA and a
RT previously unrecognized gene tldD, in the control of DNA gyrase by
RT lsdD (ccdB) of sex factor F."
RL J. Mol. Biol. 256:483-502(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RC MEDLINE=21074935; PubMed=11206551;

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RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobdec E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7."
RT Nature 409:529-533(2001).
RL
RN
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RMD 0509952;
RC MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -1- SIMILARITY: STRONG, TO H. INFLUENZAЕ H1151.
-----
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-----
CC EMBL: M95096; AAA24760.1; -
CC EMBL: U14003; AAA97131.1; -
CC EMBL: AE000494; AAC77191.1; -
CC EMBL: D44452; BAA07914.1; -
CC EMBL: AE005655; AAG59431.1; -
CC EMBL: AP002568; BAB38634.1; -
CC Ecogene: EG11410; yj9A.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 15 23 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 183 AA; 21359 MW; 069CF47719CD59CB CRC64;
Query Match 1.2%; Score 7; DB 1; Length 183;
Best local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 133 RQALDKL 139
| | | | |
Db 98 RQALDKL 104
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RESULT 14
CIT1_MOUSE STANDARD: PRT; 203 AA.
ID CIT1_MOUSE
AC P97769;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cbp/p300-Interacting transactivator 1 (Melanocyte-specific protein 1).
GN CITFD1 OR MS31.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97057236; PubMed=8901575;
RA Shida T., Fenner M.H., Isselbacher K.J.;
RT "msg1, a novel melanocyte-specific gene, encodes a nuclear protein
RT and is associated with pigmentation."
RT Proc. Natl. Acad. Sci. U.S.A. 93:12298-12303(1996).
CC -1- FUNCTION: NOT KNOWN. SEEMS TO BE ASSOCIATED WITH PIGMENTATION.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN MELANOCYTES AND TESTIS.
CC EXPRESSED AT HIGH LEVELS IN THE STRONGLY PIGMENTED MELANOMA CELLS

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CC      BUT AT LOW LEVELS IN THE WEAKLY PIGMENTED CELLS.
CC      -1- SIMILARITY: BELONGS TO THE CITED FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: U65091; AAC53048.1;
CC      MCD: MCD:108023; Cited1.
CC      Nucleic Protein: 159
CC      DOMAIN 159
CC      SEQUENCE 203 AA: 20800 MW; BE968A5182873003 CRC64;
CC
CC      Query Match
CC      Best Local Similarity 100.0%; Score 7; DB 1; Length 203;
CC      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      OY 183 GSPGSVS 189
CC      DB 141 GSPGSVS 147
CC
CC      RESULT 15
CC      YX26_MYCTU STANDARD: PRT: 232 AA.
CC      ID 050702:
CC      DT 01-NOV-1997 (Rel. 35, Created)
CC      DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC      DE Hypothetical PPE-family protein RV3426.
CC      GN RV3426 OR MYCY78.03C.
CC      OS Mycobacterium tuberculosis.
CC      Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales; Mycobacteriaceae; Mycobacterium.
CC      NCBI_Taxid:1773;
CC      RN 11
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN-H37RV;
CC      RX MEDLINE-98255987; PubMed-9634230;
CC      RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
CC      Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
CC      Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
CC      Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
CC      Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
CC      Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
CC      Rutherford S., Seeger K., Skelton S., Squares S., Squares R.,
CC      Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
CC      RT "Deciphering the biology of Mycobacterium tuberculosis from the
CC      complete genome sequence."
CC      RL Nature 393:537-544(1998).
CC      -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
CC      EMBL: Z77165; CAB01030.1;
CC      Tuberculin: RV3426;
CC      InterPro: IPR000030; Microbac_PPE.
CC      Pfam: PF00823; PPE; 1
CC      Hypothetical protein: Complete proteome.
CC      SEQUENCE 232 AA: 25872 MW; D76512D49EB272C6 CRC64;
CC
CC      Query Match
CC      Best Local Similarity 100.0%; Score 7; DB 1; Length 232;
CC      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      OY 168 PRGRRL 174
CC      DB 179 PRGRRL 185
CC
CC      Search completed: April 16, 2003, 16:35:19
CC      Job time : 37.4729 secs
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Oy	1	MLKXITGLSNNAPADGDESIFKPAKI	PVSGPFLYVTCGVDDCPDSSMAKIRALISGK	60
Dp	1	MMKXLYIGLNSENAPADGESIFKPAKI	PVSGPFLYVTCGVAVDDCPDSSMAKIRALISGK	60
Oy	61	IELHCKP1EYVHSHVPRROB1RKLQJRNPHI	LOMEVLOSILVOYGVSCEQVYNDSETA	120
Dp	61	IELHCKP1EYVHSHVPRROB1RKLQJRNPHI	LOMEVLOSILVOYGVSCEQVYNDSETA	120
Oy	121	VYNNVYSSKQDAQALDKNGOLENPLTKVAIT	PDMAAQONLQOPKRGRLGROSS	180
Dp	121	VYNNVYSSKQDAQALDKNGOLENPLTKVAIT	PDMAAQONLQOPKRGRLGROSS	180
Oy	181	ROGSGCSYKRCQDPLPLALVPQVGAITGEGAT	TRNTKOTOSKIDYHREKACAA	240
Dp	181	ROGSGCSYKRCQDPLPLALVPQVGAITGEGAT	TRNTKOTOSKIDYHREKACAA	240
Oy	241	EXSTITLSTPBGISAAKCSILEIMHKEKODIKTE	ETPKLILAHNNVGLRIGKGRNLK	300
Dp	241	EXSTITLSTPBGISAAKCSILEIMHKEKODIKTE	ETPKLILAHNNVGLRIGKGRNLK	300
Oy	301	KIEODTQKTTISPLQELTUPPERTITVKGAN	ETCAKAEELMKKIRRESYENDIASNL	360
Dp	301	KIEODTQKTTISPLQELTUPPERTITVKGAN	ETCAKAEELMKKIRRESYENDIASNL	360
Oy	361	QAHILPEGLNALGALPEPTSGMPPTSGPSSANT	PRYQDFROSETEVHOPIPALSVAI	420
Dp	361	QAHILPEGLNALGALPEPTSGMPPTSGPSSANT	PRYQDFROSETEVHOPIPALSVAI	420
Oy	421	ICKGCOHITKOLSRPAGASIKIAPADAPDAV	VRNVIITGPPEAOFRACGIRYKIKEENFV	480
Dp	421	ICKGCOHITKOLSRPAGASIKIAPADAPDAV	VRNVIITGPPEAOFRACGIRYKIKEENFV	480
Oy	481	SREBEVKLEAHIRVPSFAAGRYIGKGSKTVEL	LONLSSAEVYVPRDQTPENDQVYVKIT	540
Dp	481	SREBEVKLEAHIRVPSFAAGRYIGKGSKTVEL	LONLSSAEVYVPRDQTPENDQVYVKIT	540
Oy	541	GHFYACQVQARKIOETILTOVKHOQAKALQSG	PPSORRK	579
Dp	541	GHFYACQVQARKIOETILTOVKHOQAKALQSG	PPSORRK	579

RESULT 2	PRELIMINARY:	PRT:	579 AA.
09CENB8			
ID	09CENB8		
AC	09CENB8:		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	10 days embryo cDNA, RIKEN full-length enriched library,		
DE	clone:2610036B18, full insert sequence (Igf2 mRNA-binding protein		
GN	IGFBP3 OR 261010111R1X OR MIMF3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NC	NCBI_TaxId:10090;		
RN			
RP	SEQUENCE FROM N.A.		
RC	STRAIN-C57BL/6J; TISSUE-EMBRYO:		
RX	MEDLINE-21085660; PubMed-11217831;		
RA	Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Atakawa T., Hata A., Fukunishi Y., Kono H., Adachi T., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,		
RA	Saito T., Ozakaki Y., Gotohori T., Bono H., Katsukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batzliov S., Casavant T.,		
RA	Kueth P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schmiel L.M., Stabali F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J.D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Grossstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gastreich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		

RA	Lyons P., Marchionni L., Mashima J., Mezzarelli J., Mommaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaeli H., Sato K., Schoenbach C., Seya T., Shibaoka Y., Storch K.-F.,
RA	Suzuki H., Toyokura K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA	Hayashizaki Y.
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
RN	12]
RP	SEQUENCE FROM N.A.
RA	Mori H., Sakakibara S., Imai T., Nakamura Y., Iijima T., Suzuki A.,
RA	Yasui Y., Takeda M., Okano H.;
RT	"Expression of mouse Igf2 mRNA-binding protein 3 and its implications
RT	for the developing central nervous system.";
RL	J. Neurosci. Res. 0:0-0(2001).
DR	EMBL: AK011689; BAB2779.1; -
DR	EMBL: AB046173; BAB19755.1; -
DR	MOD: MGI:1890359; Igf2bp3.
DR	InterPro: IPR004087; KH_dom.
DR	InterPro: IPR004088; KH_type.1.
DR	InterPro: IPR000504; RNA_rec_mot.
DR	Pfam: PF00013; KH-domain.4.
DR	Pfam: PF00076; rrm.2.
DR	SMART: SM00332; KH.4.
DR	SMART: SM00360; RRM.2.
DR	PROSITE: PS50084; KH_type.1; 4.
DR	PROSITE: PS50102; RRM.2.
DR	SEQUENCE 579 AA; 63574 MW; CABD9A4155B932B7 CRC64;

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Qy      411  FLPALSVATIGKGGOHKILSRFAGSASIKTAPAEAPADAKVPMVITITSPAPAKKGGRI 470
Db      411  FLPALSVATIGKGGOHKILSRFAGSASIKTAPAEAPADAKVPMVITITSPAPAKKGGRI 470
Qy      471  YKRIEENFVSPEKVEKLEMHIRVSPFAAGNVIGKGGKIVNELQ 514
Db      471  YKRIEENFVSPEKVEKLEMHIRVSPFAAGNVIGKGGKIVNELQ 514

RESULT 3
057526      PRELIMINARY:      PRT:      593 AA.
AC      057526:
DT      01-JUN-1998 (TREMblrel, 06, Created)
DT      01-JUN-1998 (TREMblrel, 06, Last sequence update)
DT      01-JUN-2002 (TREMblrel, 21, Last annotation update)
DE      KH domain-containing transcription factor B3.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92249652; PubMed=1577195;
RA      Pfaff S.L., Taylor W.L.;
RT      "Characterization of a Xenopus oocyte factor that binds to a
RT      developmentally regulated cis-element in the PIIIA gene.",
RL      Dev. Biol. 151:306-316(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Griffin D., Taylor W.L.;
RL      Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Havin L., Gile A., Elisha Z., Oberman F., Yaniv K.,
RA      Pressman Schwartz S., Standart N.M., Yisraeli J.K.;
RL      Genes Dev. 0:0-0(1998).
DR      EMBL; AF042353; AAC97457.1; -
DR      EMBL; AF064633; AAC18597.1; -

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DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 593 AA; 65385 MW; 5A5AE4B4A1D55DF7 CRC64;

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 KFEETPLKILAHNNFVGRLLGKESGRNKKTEODTFRITISPLQ 316  
 DB 281 KFEETPLKILAHNNFVGRLLGKESGRNKKTEODTFRITISPLQ 325

RESULT 4  
 073932 PRELIMINARY; PRT; 594 AA.

AC 073932;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Vg1 RNA binding protein variant D.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NC NCBITaxid=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Havin L., Glt A., Elisha Z., Oberman F., Yaniv K.,  
 RA Pressman Schwartz S., Standard N.M., Yisraeli J.K.;  
 RL Genes Dev. 0:0-0(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-9828351; PubMed-9560341;  
 RA Deslier J.O., Highett M.I., Abramson T., Schnapp B.J.;  
 RT "A highly conserved RNA-binding protein for cytoplasmic mRNA  
 localization in vertebrates."  
 RL Curr. Biol. 8:489-496(1998).  
 DR EMBL: AF064634; AAC18598.1; -.  
 DR EMBL: AF055923; AAC1285.1; -.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 594 AA; 65643 MW; 5ACEN7BF0856DD6 CRC64;

Query Match  
 Best Local Similarity 7.8%; Score 45; DB 13; Length 594;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 KFEETPLKILAHNNFVGRLLGKESGRNKKTEODTFRITISPLQ 316  
 DB 282 KFEETPLKILAHNNFVGRLLGKESGRNKKTEODTFRITISPLQ 326

RESULT 5  
 09PW80 PRELIMINARY; PRT; 582 AA.  
 AC 09PW80;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Vg1 RNA binding protein.  
 GN DVRI8BP.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBITaxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Zhang Q., Yaniv K., Oberman F., Wolke U., Glt A., Fromer M.,  
 RA Taylor W., Meyer D., Standard N., Raz E., Yisraeli J.K.;  
 RT "Vg1 RBP intracellular distribution and evolutionarily conserved  
 RT expression suggest multiple roles during development."  
 RL Mech. Dev. 0:0-0(1999).  
 DR EMBL: AF161270; AAD45610.1; -.  
 DR ZFIN: ZDB-GENE-000308-1; dvrlbp.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR InterPro: IPR000504; RNA\_type\_1.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 SO SEQUENCE 582 AA; 63351 MW; 9DAE63200681B306 CRC64;

Query Match  
 Best Local Similarity 7.4%; Score 43; DB 13; Length 582;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 274 TEETPLKILAHNNFVGRLLGKESGRNKKTEODTFRITISPLQ 316  
 DB 273 TEETPLKILAHNNFVGRLLGKESGRNKKTEODTFRITISPLQ 315

RESULT 6  
 042254 PRELIMINARY; PRT; 576 AA.  
 AC 042254;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Zipcode binding protein.  
 GN ZBP1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NC NCBITaxid=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-9722007; PubMed-9121465;  
 RA Ross A.F., Oleynikov Y.S., Kislauskis E.H., Tanaja K.L., Singer R.H.;  
 RT "Characterization of a beta-actin mRNA zipcode-binding protein."  
 RL Mol. Cell. Biol. 17:2158-2165(1997).  
 DR EMBL: AF026527; AAB62299.1; -.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 576 AA; 63271 MW; 01AAE2D1D81C8811 CRC64;

Query Match  
 Best Local Similarity 6.2%; Score 36; DB 13; Length 576;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 VGATGEGATIRNTKOTOSKIDVHRKKNAGAAR 242
    |||||
DB 207 VGATGEGATIRNTKOTOSKIDVHRKKNAGAAR 242

RESULT 7
O9NZ18 PRELIMINARY: PRT: 577 AA.
AC O9NZ18:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE mRNA-binding protein CRDBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ioannidis P., Trangas T., Dimitriadis E., Samiotaki M.,
RA Panousakopoulos G., Kyriazoglou I., Voutoulas S., Tsipalis C.M.,
RA Kitas C., Aganitis N., Pandis N.;
RT "Ectopic expression of a KH-domain containing protein, highly
RT homologous to both human IMP-1 and mouse CRD-BP, in benign and
RT malignant mesenchymal tumors."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF198254; AAF37203.1;
DR HSSP: P11940; ICVJ.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR004088; KH_type_1.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00013; KH-domain; 4.
DR Pfam: PF00076; rtm; 2.
DR SMART: SM00322; KH; 4.
DR SMART: SM00360; RRM; 2.
DR PROSITE: PS50084; KH_type_1; 4.
DR PROSITE: PS50102; RRM; 2.
SQ SEQUENCE 577 AA; 63456 MW; 0749A060F252D81D CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 4; Length 577;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 VGATGEGATIRNTKOTOSKIDVHRKKNAGAAR 242
    |||||
DB 207 VGATGEGATIRNTKOTOSKIDVHRKKNAGAAR 242

RESULT 8
O88477 PRELIMINARY: PRT: 577 AA.
ID O88477:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coding region determinant binding protein (Coding region determinant-
DE binding protein).
DE Ige2Bp1 OR CRDBP.
GN Ige2Bp1 OR CRDBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92217743; PubMed=1559612;
RA Bernstein P.L., Herrick D.J., Prokipcak R.D., Ross J.;
RT "Control of c-myc mRNA half-life in vitro by a protein capable of
RT binding to a coding region stability determinant."
RL Genes Dev. 6:642-654(1992).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE=94158886; PubMed=8114742;
RA Herrick D.J., Ross J.;
RT "The half-life of c-myc mRNA in growing and serum-stimulated cells:
RT influence of the coding and 3' untranslated regions and role of
RT ribosome translocation."
RL Mol. Cell. Biol. 14:2119-2128(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=94179348; PubMed=8132663;
RA Prokipcak R.D., Herrick D.J., Ross J.;
RT "Purification and properties of a protein that binds to the C-terminal
RT coding region of human c-myc mRNA."
RL J. Biol. Chem. 269:9261-9269(1994).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=97322234; PubMed=9178888;
RA Leeds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.;
RA Gruppso P.A., Ross J.;
RT "Developmental regulation of CRD-BP, an RNA-binding protein that
RT stabilizes c-myc mRNA in vitro."
RL Oncogene 14:1279-1286(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ross J., Prokipcak R.D., Leeds P., Doyle G.A.R., Betz N.A.,
RA Fleisig A.J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Funada S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Tomita M., Wagner L.,
RA Schiomi L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AF061569; AAC72743.1;
DR EMBL: AK013940; BAB29071.1;
DR HSSP: P11940; ICVJ.
DR MGD: MGI:1890357; Ige2Bp1.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR004088; KH_type_1.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00013; KH-domain; 4.
DR Pfam: PF00076; rtm; 2.
DR SMART: SM00322; KH; 4.
DR SMART: SM00360; RRM; 2.
DR PROSITE: PS50084; KH_type_1; 4.
DR PROSITE: PS50102; RRM; 2.
SQ SEQUENCE 577 AA; 63450 MW; EFB1AF2F9F0344 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 11; Length 577;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 VGATGEGATIRNTKOTOSKIDVHRKKNAGAAR 242
    |||||
DB 207 VGATGEGATIRNTKOTOSKIDVHRKKNAGAAR 242

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RESULT 9
ID Q9D054 PRELIMINARY; PRT; 100 AA.
AC Q9D054;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2002 (TREMBlrel. 17, Last sequence update)
DE 2610101N1R1K protein.
GN IGF2BP3 OR 2610101N1R1K.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawal J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guslinch S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK011797; BAB27848.1; -
DR MGD: MGI:1890359; Igf2bp3.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR SMART: SM00360; rrm; 1.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 100 AA; 11249 MW; 4D871E37EB9D5466 CRC64;

Query Match 4.7%; Score 27; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 EVEHSVPKRRIRKLQIRNIPHLQWE 95
Db 69 EVEHSVPKRRIRKLQIRNIPHLQWE 95

RESULT 10
ID Q9Y6M1 PRELIMINARY; PRT; 556 AA.
AC Q9Y6M1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hepatocellular carcinoma autoantigen.
GN P62.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99207072; PubMed=10190901;
RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;
RA "A novel cytoplasmic protein with RNA-binding motifs is an autoantigen
RT

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RT in human hepatocellular carcinoma.";
RL J. Exp. Med. 189:1101-1110(1999).
DR EMBL: AF057352; AAD31596.1; -
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR004088; KH_type_1.
DR InterPro: IPR00504; RNA_rec_mot.
DR Pfam: PF00013; KH-domain; 4.
DR Pfam: PF00076; rrm; 2.
DR SMART: SM00322; KH; 4.
DR SMART: SM00360; RRM; 2.
DR PROSITE: PS50084; KH_TYPE_1; 4.
DR PROSITE: PS50102; RRM; 2.
SQ SEQUENCE 556 AA; 61842 MW; 1EDFB100443DDC4 CRC64;

Query Match 3.3%; Score 19; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 RNVITGPPEAOFKAGRI 470
Db 431 RNVITGPPEAOFKAGRI 449

RESULT 11
ID Q9MTM6 PRELIMINARY; PRT; 84 AA.
AC Q9MTM6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 9.7 kDa protein.
OS Oenothera hookeri (Hooker's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.
ON NCBI_TaxID=85636;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309318; PubMed=10852478;
RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
RA Chiu W.L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT Enoenothera plastomes.";
RL Mol. Gen. Genet. 263:581-585(2000).
DR EMBL: AJ271079; CAB67150.1; -
DR Chloroplast; Hypothetical protein.
SQ SEQUENCE 84 AA; 9674 MW; D37B6A918546E0CB CRC64;

Query Match 1.4%; Score 8; DB 8; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 MNLQAHLI 365
Db 1 MNLQAHLI 8

RESULT 12
ID Q8TXJ1 PRELIMINARY; PRT; 142 AA.
AC Q8TXJ1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Transcription elongation factor NUSA.
GN NUSA_1 OR MK0682.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
ON NCBI_TaxID=2320;
RN [1]

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RP SEQUENCE FROM N.A.  
 RC STRAIN-AV19 / DSM 6324 / JCM 9639;  
 RX MEDLINE-21927647; PubMed-11930014;  
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,  
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
 RA Nalekh A.G., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
 RA Mal'kh A.G., Koonin E.V., Koz'yavkin S.A.;  
 RT "The complete genome of hyperthermophilic Methanopyrus kandleri AV19  
 RT and monophyly of archaeal methanogens.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
 KW EMBL: AE010361; AAM01897.1;  
 DR Elongation factor: Complete proteome.  
 SO SEQUENCE 142 AA; 15909 MW; BF4FFEC4E03B2677 CRC64;

Query Match 1.4%; Score 8; DB 17; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 GRVYKGG 507  
 |||||  
 Db 113 GRVYKGG 120

RESULT 13  
 ID O9BIJ0 PRELIMINARY; PRT: 152 AA.  
 AC O9BIJ0;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE Putative RNA-binding protein (Fragment).  
 OS Patella vulgata (Common limpet).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;  
 OC Patelioidea; Patelidae; Patella.  
 OX NCBI\_TaxID=6465;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Klerck A.H.E.M., de Boer E., van Loon A.E.;  
 RT "Spatio-temporal expression of a gene encoding a putative RNA-binding  
 RT protein during the early larval development of the mollusc Patella  
 RT vulgata.";  
 RL Dev. Genes Evol. 0:0-0(2001).  
 DR EMBL: AF61436; AAK32728.1;  
 DR InterPro: IPR002952; Eggshell.  
 DR InterPro: IPR004088; KH\_dom.  
 DR Pfam: PF00013; KH-domain\_1.  
 DR PRINTS: PR01228; EGGSHELL.  
 DR SMART: SM00322; KH.1.  
 DR PROSITE: PS50084; KH\_Type\_1; 1.  
 DR NON\_TER 1  
 SQ SEQUENCE 152 AA; 15181 MW; 2950AB44E754F97 CRC64;

Query Match 1.4%; Score 8; DB 5; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 GRVYKGG 507  
 |||||  
 Db 42 GRVYKGG 49

RESULT 14  
 ID O97KZ6 PRELIMINARY; PRT: 242 AA.  
 AC O97KZ6;  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Glycerol uptake facilitator protein, permease.  
 GN CAG0770  
 OS Clostridium acetobutylicum  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

OC Clostridiales; Clostridiaceae; Clostridium.  
 OX NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE-21359325; PubMed-11465286;  
 RA Nieling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng O.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Benmelt G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum.";  
 RL J. Bacteriol. 183:4823-4838(2001).  
 DR EMBL: AE007592; AAK78746.1;  
 DR InterPro: IPR000425; MIP\_family.  
 DR Pfam: PF00230; MIP.1.  
 DR PRINTS: PR00783; MIPTRNSICP.  
 DR PRODOM: PD000295; MIP\_family.1.  
 DR PROSITE: PS00221; MIP; UNKNOWN\_1.  
 DR Complete proteome.  
 SO SEQUENCE 242 AA; 25807 MW; 26E7A62AE7377AF CRC64;

Query Match 1.4%; Score 8; DB 16; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 QFVGAIIG 212  
 |||||  
 Db 94 QFVGAIIG 101

RESULT 15  
 ID Q9SSZ7 PRELIMINARY; PRT: 318 AA.  
 AC Q9SSZ7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Peroxidase 3.  
 OS Scutellaria baicalensis.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asterales; easterids I; Lamiales; Lamiales; Scutellaria.  
 OX NCBI\_TaxID=65409;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99403061; PubMed-10473572;  
 RA Morimoto S., Tateishi N., Inuyama M., Taura F., Tanaka H., Shoyama Y.;  
 RT "Identification and molecular characterization of novel peroxidase  
 RT with structural protein-like properties.";  
 RL J. Biol. Chem. 274:26192-26198(1999).  
 DR EMBL: AB024439; BAA7389.1;  
 DR HSSP: P22195; ISCH.  
 DR InterPro: IPR002016; Peroxidase.  
 DR Pfam: PF00141; peroxidase.1.  
 DR PRINTS: PR00458; PEROXIDASE.  
 DR PROSITE: PS00435; PEROXIDASE\_1; 1.  
 DR PROSITE: PS00436; PEROXIDASE\_2; 1.  
 SQ SEQUENCE 318 AA; 33903 MW; 6CDD0DA3FE470C83 CRC64;

Query Match 1.4%; Score 8; DB 10; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 366 PGJLNAL 373  
 |||||  
 Db 165 PGJLNAL 172

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 Job time: 74.3547 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:18:40 ; Search time 32.3251 Seconds

(without alignments)  
527.016 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 2956

Sequence: 1 MNKLYIGNLSENAPSDLES.....VKHQOQKALQSGPPOSRRK 579

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA: \*  
2: /cgn2\_6/prodata/1/1aa/5A.COMB.pep: \*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/prodata/1/1aa/6C.COMB.pep: \*  
6: /cgn2\_6/prodata/1/1aa/6D.COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2956	100.0	579	4 US-09-643-597-176	Sequence 176, App
2	2943	99.6	579	4 US-09-643-597-348	Sequence 348, App
3	2190	74.1	577	4 US-09-261-855-2	Sequence 2, App11
4	241	8.2	644	1 US-08-021-608D-2	Sequence 2, App11
5	241	8.2	644	1 US-08-726-160-2	Sequence 2, App11
6	241	8.2	644	5 PCT-US94-01782-2	Sequence 2, App11
7	238	8.1	49	4 US-09-261-855-22	Sequence 22, App1
8	227	8.0	48	4 US-09-261-855-24	Sequence 24, App1
9	236.5	8.0	643	1 US-08-021-608D-10	Sequence 10, App1
10	236.5	8.0	643	1 US-08-726-160-10	Sequence 10, App1
11	236.5	8.0	643	5 PCT-US94-01782-10	Sequence 10, App1
12	232	7.8	49	4 US-09-261-855-18	Sequence 18, App1
13	229.5	7.8	590	1 US-08-021-608D-8	Sequence 8, App11
14	229.5	7.8	590	1 US-08-726-160-8	Sequence 8, App11
15	229.5	7.8	590	5 PCT-US94-01782-8	Sequence 8, App11
16	227	7.7	47	4 US-09-261-855-23	Sequence 23, App1
17	227	7.7	530	4 US-08-187-793-4	Sequence 4, App1
18	225	7.6	47	4 US-09-261-855-21	Sequence 21, App1
19	219	7.4	48	4 US-09-261-855-20	Sequence 20, App1
20	218	7.4	47	4 US-09-261-855-17	Sequence 17, App1
21	190	6.4	47	4 US-09-261-855-19	Sequence 19, App1
22	159.5	5.4	471	4 US-08-866-928B-1	Sequence 1, App11
23	154	5.2	343	1 US-08-187-793-2	Sequence 2, App11
24	147	5.0	243	1 US-08-021-608D-6	Sequence 6, App11
25	147	5.0	243	1 US-08-726-160-6	Sequence 6, App11
26	147	5.0	243	5 PCT-US94-01782-6	Sequence 6, App11
27	146.5	5.0	688	4 US-08-973-273-26	Sequence 26, App11

28	146.5	5.0	747	4 US-08-973-273-3	Sequence 3, App11
29	145.5	4.9	414	1 US-07-667-276A-4	Sequence 4, App1
30	140.5	4.6	655	4 US-09-347-833-4	Sequence 4, App1
31	139	4.7	444	1 US-07-881-075-3	Sequence 3, App1
32	139	4.7	444	1 US-08-120-827-3	Sequence 3, App11
33	139	4.7	444	1 US-08-478-675-3	Sequence 3, App11
34	133.5	4.5	359	1 US-07-881-075-2	Sequence 2, App11
35	133.5	4.5	359	1 US-08-120-827-2	Sequence 2, App11
36	133.5	4.5	359	1 US-08-478-675-2	Sequence 2, App11
37	133	4.5	380	1 US-07-881-075-51	Sequence 51, App1
38	133	4.5	380	1 US-08-120-827-51	Sequence 51, App1
39	133	4.5	380	1 US-08-478-675-51	Sequence 51, App1
40	132	4.5	443	2 US-08-935-450-6	Sequence 6, App1
41	129.5	4.4	545	2 US-08-990-114-1	Sequence 6, App1
42	129.5	4.4	545	2 US-09-241-333-1	Sequence 1, App11
43	129	4.4	652	4 US-08-973-273-5	Sequence 5, App11
44	127	4.3	652	4 US-09-347-833-2	Sequence 2, App11
45	122.5	4.1	428	4 US-09-347-833-6	Sequence 6, App11

## ALIGNMENTS

RESULT 1	US-09-643-597-176		
Sequence 176, App1	Application US/09643597		
Patent No. 6426072			
GENERAL INFORMATION:			
APPLICANT: Wang, Tonglong			
APPLICANT: Fan, Liqun			
APPLICANT: Kalos, Michael D.			
APPLICANT: Bangur, Chaitanya S.			
APPLICANT: Hosken, Nancy			
APPLICANT: Fanger, Gary R.			
APPLICANT: Li, Samuel X.			
APPLICANT: Wang, Aijun			
APPLICANT: Skelky, Yasir A.W.			
APPLICANT: Henderson, Robert A.			
APPLICANT: McNeill, Patricia D.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
FILE REFERENCE: 210121.455C11			
CURRENT APPLICATION NUMBER: US/09/643,597			
CURRENT FILING DATE: 2000-08-21			
NUMBER OF SEQ ID NOS: 369			
SOFTWARE: FASTSEQ for Windows Version 3.0			
SEQ ID NO 176			
LENGTH: 579			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-643-597-176			
Query Match	100.0%	Score 2956, DB 4; Length 579;	
Best Local Similarity	100.0%	Pred. No. 1.7e-255;	
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MNKLYIGNLSENAPSDLESIFPKDKIPYSGPPLVTKGYAFVDCDESMALKALAEALSK 60		
DB	1 MNKLYIGNLSENAPSDLESIFPKDKIPYSGPPLVTKGYAFVDCDESMALKALAEALSK 60		
QY	61 IELHKEPFEVSHVSPKQRIKQIRNIPPHLOMEVLSLVLQYGVSVCSQVNTDSETA 120		
DB	61 IELHKEPFEVSHVSPKQRIKQIRNIPPHLOMEVLSLVLQYGVSVCSQVNTDSETA 120		
QY	121 VVNVTVSSKDDARALDKLNGFLENPTLKVAITPEMAAQQNPLOQPRGRGRGIGOGSS 180		
DB	121 VVNVTVSSKDDARALDKLNGFLENPTLKVAITPEMAAQQNPLOQPRGRGRGIGOGSS 180		
QY	181 RQSGFVSVKQPCDPLRLVLPQFVGALIGKEGATIRNTKQTSKIDVHRKNGAA 240		
DB	181 RQSGFVSVKQPCDPLRLVLPQFVGALIGKEGATIRNTKQTSKIDVHRKNGAA 240		
QY	241 EKSTIILSTPGSTAACKSILIEIMHKEADIKFTEIEIPKILAHNNFVGRIGKEGRNLK 300		

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Db 241 EKSTITLSTPECTSAACKSILEIMHKEADIKFTBEIPDKTLAHNNFVGRIGKGRRLK 300
OY 301 KIEODTDTKITITSPLOEELTYNPERTITVKGWETCAKAEEMIMKIRESENDIASNML 360
Db 301 KIEODTDTKITITSPLOEELTYNPERTITVKGWETCAKAEEMIMKIRESENDIASNML 360
OY 361 QAHILPGILNMLNGLFPTSGMPPTSGPPSAMTPPYPOFESSTETVHOEIPALSVGAI 420
Db 361 QAHILPGILNMLNGLFPTSGMPPTSGPPSAMTPPYPOFESSTETVHOEIPALSVGAI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITTPPEAOFKAOGRIYKIKEENFV 480
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITTPPEAOFKAOGRIYKIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPOTPDENDQVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPOTPDENDQVYVKIT 540
OY 541 GHFYACOVAORRKOIEILITOVKOHQOKALQSGPPQSRK 579
Db 541 GHFYACOVAORRKOIEILITOVKOHQOKALQSGPPQSRK 579

```

## RESULT 2

```

US-09-643-597-348
? Sequence 348, Application US/09643597
? Patent No. 6426072
? GENERAL INFORMATION:
? APPLICANT: Wang, Tongtong
? APPLICANT: Fan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aljun
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.453C11
? CURRENT APPLICATION NUMBER: US/09/643,597
? CURRENT FILING DATE: 2000-08-21
? NUMBER OF SEQ ID NOS: 369
? SOFTWARE: SEQ ID NOS: 369
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 348
? LENGTH: 579
? TYPE: Protein
? ORGANISM: Homo sapiens
US-09-643-597-348

```

```

Query Match 99.6%: Score 2943; DB 4; Length 579;
Best Local Similarity 99.7%: Pred. No. 2, 4e-254;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVYTGTAFTDCDSEWALKALIALSGK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVYTGTAFTDCDSEWALKALIALSGK 60
OY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVQYVSGEONVNDSETA 120
Db 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVQYVSGEONVNDSETA 120
OY 121 VVAVTTSSKQARQALDKINGFOLNFTLKVAITPDEMAAQNPLQDPRGRGLGQGRSS 180
Db 121 VVAVTTSSKQARQALDKINGFOLNFTLKVAITPDEMAAQNPLQDPRGRGLGQGRSS 180
OY 181 ROGSPGYSKOKPCDPLPLVLPPOFGAIIKGGATTNTIKOTOSTIDYHKKENAGA 240
Db 181 ROGSPGYSKOKPCDPLPLVLPPOFGAIIKGGATTNTIKOTOSTIDYHKKENAGA 240

```

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OY 241 EKSTITLSTPECTSAACKSILEIMHKEADIKFTBEIPDKTLAHNNFVGRIGKGRRLK 300
Db 241 EKSTITLSTPECTSAACKSILEIMHKEADIKFTBEIPDKTLAHNNFVGRIGKGRRLK 300
OY 301 KIEODTDTKITITSPLOEELTYNPERTITVKGWETCAKAEEMIMKIRESENDIASNML 360
Db 301 KIEODTDTKITITSPLOEELTYNPERTITVKGWETCAKAEEMIMKIRESENDIASNML 360
OY 361 QAHILPGILNMLNGLFPTSGMPPTSGPPSAMTPPYPOFESSTETVHOEIPALSVGAI 420
Db 361 QAHILPGILNMLNGLFPTSGMPPTSGPPSAMTPPYPOFESSTETVHOEIPALSVGAI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITTPPEAOFKAOGRIYKIKEENFV 480
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITTPPEAOFKAOGRIYKIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPOTPDENDQVYVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPOTPDENDQVYVKIT 540
OY 541 GHFYACOVAORRKOIEILITOVKOHQOKALQSGPPQSRK 579
Db 541 GHFYACOVAORRKOIEILITOVKOHQOKALQSGPPQSRK 579

```

## RESULT 3

```

US-09-261-855-2
? Sequence 2, Application US/09261855A
? Patent No. 6255055
? GENERAL INFORMATION:
? APPLICANT: Ross, Jeffrey
? TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
? TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
? FILE REFERENCE: 960296.95131
? CURRENT APPLICATION NUMBER: US/09/261,855A
? CURRENT FILING DATE: 1999-03-03
? NUMBER OF SEQ ID NOS: 46
? SOFTWARE: Patentia Ver. 2.0
? SEQ ID NO 2
? LENGTH: 577
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-261-855-2

```

```

Query Match 74.1%: Score 2190; DB 4; Length 577;
Best Local Similarity 74.1%: Pred. No. 4, 3e-187;
Matches 434; Conservative 62; Mismatches 74; Indels 16; Gaps 8;

```

```

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVYTGTAFTDCDSEWALKALIALSGK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVYTGTAFTDCDSEWALKALIALSGK 60
OY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVQYVSGEONVNDSETA 120
Db 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOMEVLDLSLVQYVSGEONVNDSETA 120
OY 121 VVAVTTSSKQARQALDKINGFOLNFTLKVAITPDEMAAQNPLQDPRGRGLGQGRSS 179
Db 121 VVAVTTSSKQARQALDKINGFOLNFTLKVAITPDEMAAQNPLQDPRGRGLGQGRSS 176
OY 180 SRQSP--GYSKOKPCDPLPLVLPPOFGAIIKGGATTNTIKOTOSTIDYHKKEN 236
Db 180 SRQSP--GYSKOKPCDPLPLVLPPOFGAIIKGGATTNTIKOTOSTIDYHKKEN 236
OY 237 AGAAEKSITLSTPECTSAACKSILEIMHKEADIKFTBEIPDKTLAHNNFVGRIGKGR 296
Db 237 AGAAEKSITLSTPECTSAACKSILEIMHKEADIKFTBEIPDKTLAHNNFVGRIGKGR 296
OY 297 RNLKKEODTDTKITITSPLOEELTYNPERTITVKGWETCAKAEEMIMKIRESENDIA 356
Db 297 RNLKKEODTDTKITITSPLOEELTYNPERTITVKGWETCAKAEEMIMKIRESENDIA 356
OY 357 SMLQAHILPGILNMLNGLFPTSGMPPTSGPPSAMTPPYPOFESSTETVHOEIPALSVGAI 413

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Db 357 AMSLSHILPGLNLAAGLFPASSNAVEP---PSSVTGAPRYSSEFMQAEQDMVYFIP 413
Qy 414 ALSKATITGGGCHIKQLSFPACASIKTAPAPAPKAVRYIITGPEAFKQKQITYK 473
Db 414 AQAAGATIGKGGCHIKQLSFPASASIKTAPETPSKVRMYITGPEAFKQKQITYK 473
Qy 474 IKENFVSPKEEVKLEAHIRVPSFAGRYIGKGTYNELONLSSAEVVPRDQTPDEND 533
Db 474 LKENFEGPKKEEVKLEHIRVPASAGRYIGKGTYNELONLSSAEVVPRDQTPDEND 533
Qy 534 QVVVKITGFYACQVAAQRKIQELITGVKQHQKALQSGPPQSRK 579
Db 534 QVVKITGFYASQMAQRKIRDLIAQVKQ-QHQKQ-QSNLAQARRK 577

```

# RESULT 4 US-08-021-608D-2

Sequence 2, Application US/08021608D  
Patent No. 5580760

```

GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHEICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HD60
FEATURE:
OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile
US-08-021-608D-2

```

Query Match 8.2%; Score 241; DB 1; Length 644;  
Best Local Similarity 22.3%; Pred. No. 5,66-13;  
Matches 100; Conservative 75; Mismatches 154; Indels 120; Gaps 17;

```

Qy 161 QANPLO---OPRGRGLGQGRSGSGSVSKKPCOLPLRLLYPQFVAGALIGKESAT 217
Db 63 QKRFLEDDOPDPAKAVAPWDSFTQLPRMHOQSRSVTEETVYVPGMVGFTLIGGGEQ 122
Qy 218 IRNITKQTSKIDVHKRENAGAESTITLSTPEGSTACKSILEIMKRAODIKFTE-- 275
Db 123 ISRIQESGCKIQI-APDSGGLPERSCXLTGPEVSQAKRLDQIVKRAPAGRHND 181
Qy 276 ---ELPILILANNFNWGLRIGKEGRNLKKIEDDTTKITLISPLQELTYNPERT-----I 327
Db 182 GPGNAVOCIMIPASKAGLVIGKGGETIKOLQERRAGKVMW--IOD---GPGNTGADKPL 235
Qy 328 TVKGVNTEICAAKEEIMKKIRE-----SYENDIASMNLOAILIGLNLNLGLFPPTSGM 382
Db 236 RITGDPYKVOQAKEMVELIRDQGGREVRNMGSR-----IGG-----NEGI 278
Qy 383 PPTSGPPSANTPPYQFQESFETVHOPIPLASVATIGKQGHIKQLSFPAGASIKTA 442
Db 279 DVP-----IPRFVAGIYIGNGEMIKKIKNDAGVRIQK 312
Qy 443 PAAPDAKVRMYITGPE-AQPKAO-----GRITK----- 473
Db 313 PDGTTPE-RIAQITGPPRCQHAELITDLRSVQAGNPGGPGGGRGQGMNMNG 371
Qy 474 ---IKENFVSPKEEVKLEAHIRVPSFAGRYIGKGTYNELONLSSAEVVPRDQTP 529
Db 372 PPGGLQEFNFET-----VPTGKTGLITGKGETIKISQSGARIELQHRNPP 418
Qy 530 DENDOV-VVKITGFH---FYACQVAAQRKI 553
Db 419 MADPMMKLEFTIRGTPOIDVARIQLEIKI 447

```

# RESULT 5 US-08-726-160-2

Sequence 2, Application US/08726160  
Patent No. 5734016

```

GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644

```





Db 419 NAOPNNKLETTINGTPOQIDYAROLIEKI 447

## RESULT 7

US-09-261-855-22  
Sequence 22, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: ROSS, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261.855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 49  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-261-855-22

## Query Match

Best Local Similarity 98.0%; Score 238; DB 4; Length 49;  
Pred. No. 2e-14; Mismatches 1; Indels 0; Gaps 0;

Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 281 ILAHNNFVGRLLGKGRMLKKIEODTDTKITISPLQELTLYNPRTIYV 329

Db 1 ILAHNNFVGRLLGKGRMLKKIEODTDTKITISPLQELTLYNPRTIYV 49

## RESULT 8

US-09-261-855-24  
Sequence 24, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: ROSS, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261.855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-261-855-24

## Query Match

Best Local Similarity 100.0%; Score 237; DB 4; Length 48;  
Pred. No. 2.3e-14; Mismatches 0; Indels 0; Gaps 0;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 IRVPSFAGRVIGKGGKTYNELONLSAEVYVPPDQTPPDNDVVYKI 539

Db 1 IRVPSFAGRVIGKGGKTYNELONLSAEVYVPPDQTPPDNDVVYKI 48

## RESULT 9

US-08-021-608D-10  
Sequence 10, Application US/08021608D  
Patent No. 5580760  
GENERAL INFORMATION:  
APPLICANT: LEVENS, DAVID L., DUNCAN,  
APPLICANT: ROBERT C., AND AVIGAN, MARK I.  
TITLE OF INVENTION: NOVEL FUSE BINDING  
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESS: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK

STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/021.608D  
FILING DATE: 22-FEB-1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FELLER

REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4063

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:

LENGTH: 643  
TYPE: Amino Acid

STRANDEDNESS: Single  
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide/Protein  
HYPOTHETICAL: No

ORIGINAL SOURCE:  
ORGANISM: Human

CELL LINE: HL60  
FEATURE:

OTHER INFORMATION:  
OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile

US-08-021-608D-10

Query Match  
Best Local Similarity 8.0%; Score 236.5; DB 1; Length 643;  
Pred. No. 1.4e-12; Mismatches 15; Indels 12; Gaps 16;

Matches 100; Conservative 77; Mismatches 15; Indels 12; Gaps 16;

QY 161 GONPLD---OPRRGRGIGGSSRGGSPGSVSKOPCDLPLRLVLPQFATIGKGGAT 217

Db 63 OKRPLEGDDOPDAKVAAPNDSTFGTOLP-PMHQOQBSVWTEKRYVPGCMGFTIGRGGED 121

QY 218 IRNITKOTQSKIDVHKRENGAAGKSTITLSTPEGSTAACKSILEMKKEADIKFTE-- 275

Db 122 ISRIQESGCKIQI-APDSGGLPERSCXLTGTPESVQSAKRLDQIVKGGPRAPGFHGD 180

QY 276 ---EIPKILAHNNFVGRLLGKGRMLKKIEODTDTKITISPLQELTLYNPRTIYV 327

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QY 328 TVKGNVETCAKAEELMKKTRF-----SYENDIASMNLQAHILGLNINMLGLPPTSGM 382

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QY 383 PPTSGPPSPAMTPPYPOFQSETEYVHOPILALSVGAILGKGGKHLQSLSFAGASIKTA 442

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QY 474 ---IKENFVSPKEVEKLEAHIRVPSFAGRVIGKGGKTYNELONLSAEVYVPPDQTP 529

Db 371 PPGGLQEPNFI-----VPTGKTGLIIGKGGETIKTSISQSGARIELQRNPP 417

QY 530 DENDOV-VVKITGH---FYACQVAQRT 553

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Page 6

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DB 418 NADPNMKLFTIRGTPOQIDVAROLIEKI 446

RESULT 10
US-08-726-160-10
Sequence 10, Application US/08726160
Patent No. 5734016
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C. AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 643
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HL60
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile
US-08-726-160-10

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Best Local 22.3%, Pctd No 1.4e-12,
Matches 100, Conservative 77, Mismatches 151, Indels 121, Gaps 18,

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DB 278 DVF-----IPRFVAGIYIGNGEMIKKIONAGVRIQFK 311
QY 443 PAEPAPKAVMYLITGPPE-AGFKAQ-----GRYGR-----473
DB 312 PDDSTTPE-RIMQIGPPDRQHAELITDLRSYQAQNPQGGPGRGGRGQGNMWMG 370
QY 474 ----IKENNVSPKREVKLEAHIVPSPFAGRGVIGKGTVNELONLSAEVVPDDQTP 529
DB 371 PPGDLEFNTI-----VPTGKTGLIKGGGETIKSISQSGARIETLQRPNP 417
QY 530 DENDQ-VVAKTGH----FYAQYVAQRKI 553
DB 418 NADPNMKLFTIRGTPOQIDVAROLIEKI 446

RESULT 11
PCT-US94-01782-10
Sequence 10, Application PC/TUS9401782
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01782
FILING DATE: 22-FEB-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 643
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE: HL60
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Best Local Similarity	91.8%	Pred. No.	6	7e-14			
Matches	45	Conservative	3	Mismatches	1	Indels	0
						Gaps	0

  

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 : Sequence 8, Application US/08021608D  
 : Patent No. 5580760  
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 : GENERAL INFORMATION:  
 : APPLICANT: LEVENS, DAVID L., DUNCAN,  
 : APPLICANT: ROBERT C., AND AVIGAN, MARK I.  
 : TITLE OF INVENTION: NOVEL FUSE BINDING  
 : TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
 : NUMBER OF SEQUENCES: 24  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: MORGAN & FINNEGAN  
 : STREET: 345 PARK AVENUE  
 : CITY: NEW YORK  
 : STATE: NEW YORK  
 : COUNTRY: USA  
 : ZIP: 10154  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: FLOPPY DISK  
 : COMPUTER: IBM PC COMPATIBLE  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: WORDPERFECT 5.1  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/021,608D  
 : FILING DATE: 22-FEB-1993  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER:  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: WILLIAM S. FELLER  
 : REGISTRATION NUMBER: 26,728  
 : REFERENCE/DOCKET NUMBER: 2026-4063  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 758-4800  
 : TELEFAX: (212) 751-6849  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 590  
 : TYPE: Amino Acid  
 : STRANDEDNESS: Single  
 : TOPOLOGY: Unknown  
 : MOLECULE TYPE: Peptide/Protein  
 : HYPOTHEICAL: No  
 : ORIGINAL SOURCE:  
 : ORGANISM: Human  
 : CELL LINE: HL60  
 :  
 : US-08-021-6080-8

[illegible]

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Page 8

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Qy 514 QNISAEVVPPDQTPDENDQV-VKRTGH----FYACQVQKRI 553  
Db 387 SQSGARIELOHNPENADPNMKLTIRGTPQIDYARQLIEKI 431

RESULT 14  
US08-726-160-8  
Sequence 8, Application US/08726160  
Patent No. 5714016

GENERAL INFORMATION:  
APPLICANT: LEVENS, DAVID L., DUNCAN,  
APPLICANT: ROBERT C., AND AVIGAN, MARK I.  
TITLE OF INVENTION: NOVEL FUSE BINDING  
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,160  
FILING DATE: 04-OCT-1996

CLASSIFICATION: 435  
APPLICATION NUMBER: 08/021,608  
FILING DATE: 22-FEB-1993

ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4063US1  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 590  
TYPE: Amino Acid  
STRANDEDNESS: Single  
MOLECULE TYPE: Peptide/Protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE: Human  
CELL LINE: HL60

US-08-726-160-8

Query Match 7.88; Score 229.5; DB 1: Length 590;  
Best Local Similarity 22.5%; Pctd. No. 5.2e-12;  
Matches 91; Conservative 69; Mismatches 128; Indels 117; Gaps 16;  
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Qy 262 EIMAKKADIKITE-----ELPIKILAHNNFVGRILGEGRNIAKITEQDTDTKTIISPLQ 316  
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Db 281 MIKIONDAGVRIQKPPDDGTPE-RIAQITGPPRCQHAETITDLRSVQAGNPGCG 339  
Qy 468 --GRIYK-----IKENFVSKEVEKLEAHIRVSPFAGRVIGCKGTVEL 513  
Db 340 PGRGRGRCQGMNMPPGGLQGFNFI-----VPKGTGLIGKGETIKSI 386  
Qy 514 QNISAEVVPPDQTPDENDQV-VKRTGH----FYACQVQKRI 553  
Db 387 SQSGARIELOHNPENADPNMKLTIRGTPQIDYARQLIEKI 431

RESULT 15  
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Sequence 8, Application PC/TUS9401782  
Patent No. 5714016

GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES  
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF  
HEALTH AND HUMAN SERVICES  
TITLE OF INVENTION: NOVEL FUSE BINDING  
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01782  
FILING DATE: 22-FEB-1994

CLASSIFICATION:  
APPLICATION NUMBER: U.S. 08/021,608  
FILING DATE: 22-FEB-1993

ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAM S. FEILER  
REGISTRATION NUMBER: 26,728  
REFERENCE/DOCKET NUMBER: 2026-4063PCT  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 590  
TYPE: Amino Acid  
STRANDEDNESS: Single  
MOLECULE TYPE: Peptide/Protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE: Human  
CELL LINE: HL60

US-08-726-160-8

CELL LINE: HL60  
ORGANELLE:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PCT-US94-01782-8

Query Match 7.88; Score 229.5; DB 5; Length 590;  
Best Local Similarity 22.58; Pred. No. 5.2e-12;  
Matches 91; Conservative 69; Mismatches 128; Indels 117; Gaps 16;

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DB 91 VPDGAVGFTIGRGEOISRIQDESCKIQI-APDSGILPERSCMITGTPEVSQAKRLID 149  
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QY 317 ELTVMPERT-----ITVKNVETCAKAEELMKIRE-----SYENDIASMNLQAHLP 366  
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DB 258 G-----NEGIDVP-----IPRFVGIIVIGRNGE 280  
QY 427 HIKQLSRFAGASIKITAPAEAPDAKVRVYITGPPE-AQFKAO----- 467  
DB 281 MIKKIONDAGVRIQFKPDGTPPE-RINQITGPPDRGCHMAEITDILRSVQAGNPGGPG 339  
QY 468 --GRITGK-----IKENFVSPKEEVKLEAHIRVPSFAGRVIGKGGKTYNEL 513  
DB 340 PGGRRGRGQGMNMGPPGGLQEFNFI-----VPTGKTGLIIGKGGETIKSI 386  
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DB 387 SQOSGARIEIQRNPPNADPNMKLFTIRGTPOQIDYARQLIEKI 431

Search completed: April 16, 2003, 16:23:03  
Job time : 36.3251 secs



Thu Apr 17 07:55:18 2003

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Page 1

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:19:20 : Search time 388.852 Seconds  
(without alignments)  
960.006 Million cell updates/sec

Title: US-09-897-778-176  
Perfect score: 2956  
Sequence: 1 MNKLYIGLSEMAFSDLES.....VKHQDQKALQSGPQSRK 579

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Gapop 10.0 , Gapext 0.5  
Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2956	100.0	579	18	US-09-466-396A-176	Sequence 176, App
3	2956	100.0	579	18	US-09-476-196A-176	Sequence 176, App
4	2956	100.0	579	18	US-09-480-884A-176	Sequence 176, App
5	2956	100.0	579	19	US-09-510-376A-176	Sequence 176, App
6	2956	100.0	579	19	US-09-542-615A-176	Sequence 176, App

7	2956	100.0	579	20	US-09-606-421A-176	Sequence 176, App
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9	2956	100.0	579	20 <td>US-09-630-940A-176</td> <td>Sequence 176, App</td>	US-09-630-940A-176	Sequence 176, App
10	2956	100.0	579	20 <td>US-09-630-940B-176</td> <td>Sequence 176, App</td>	US-09-630-940B-176	Sequence 176, App
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12	2956	100.0	579	20 <td>US-09-685-696-176</td> <td>Sequence 176, App</td>	US-09-685-696-176	Sequence 176, App
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14	2956	100.0	579	21 <td>US-09-791-537-49019</td> <td>Sequence 49019, A</td>	US-09-791-537-49019	Sequence 49019, A
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17	2956	100.0	579	22 <td>US-09-897-778-176</td> <td>Sequence 176, App</td>	US-09-897-778-176	Sequence 176, App
18	2956	100.0	579	24 <td>US-10-007-700-176</td> <td>Sequence 176, App</td>	US-10-007-700-176	Sequence 176, App
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28	2943	99.6	579	20 <td>US-09-662-786-348</td> <td>Sequence 348, App</td>	US-09-662-786-348	Sequence 348, App
29	2943	99.6	579	20 <td>US-09-685-696-348</td> <td>Sequence 348, App</td>	US-09-685-696-348	Sequence 348, App
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34	2943	99.6	579	22 <td>US-09-897-778-448</td> <td>Sequence 448, App</td>	US-09-897-778-448	Sequence 448, App
35	2943	99.6	579	22 <td>US-09-897-778-449</td> <td>Sequence 449, App</td>	US-09-897-778-449	Sequence 449, App
36	2943	99.6	579	24 <td>US-10-007-700-448</td> <td>Sequence 448, App</td>	US-10-007-700-448	Sequence 448, App
37	2943	99.6	579	24 <td>US-10-007-700-449</td> <td>Sequence 449, App</td>	US-10-007-700-449	Sequence 449, App
38	2943	99.6	579	25 <td>US-10-117-982-348</td> <td>Sequence 348, App</td>	US-10-117-982-348	Sequence 348, App
39	2943	99.6	579	25 <td>US-10-117-982-446</td> <td>Sequence 446, App</td>	US-10-117-982-446	Sequence 446, App
40	2943	99.6	579	25 <td>US-10-117-982-449</td> <td>Sequence 449, App</td>	US-10-117-982-449	Sequence 449, App
41	2943	99.6	579	25 <td>US-10-117-982-480</td> <td>Sequence 480, App</td>	US-10-117-982-480	Sequence 480, App
42	2943	99.6	579	25 <td>PCT-US01-47576-427</td> <td>Sequence 427, App</td>	PCT-US01-47576-427	Sequence 427, App
43	2938	99.4	586	1 <td>US-09-850-716-427</td> <td>Sequence 427, App</td>	US-09-850-716-427	Sequence 427, App
44	2938	99.4	586	22		
45	2938	99.4	586	22		

#### ALIGNMENTS

RESULT 1  
PCT-US01-47576-176  
Sequence 176 Application PC/TUS0147576  
GENERAL INFORMATION:  
APPLICANT: Cortix Corporation  
APPLICANT: Wang, Tonglong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margareta  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshinhiro  
APPLICANT: Peckman, David W.  
APPLICANT: Cal, Feng  
APPLICANT: Foy, Teresa M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE OF INVENTION: 210121.45503PC  
TITLE REFERENCE: 210121.45503PC  
CURRENT APPLICATION NUMBER: PCT/US01/47576  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-us01-47576-176

Query Match
Best Local Similarity 100.0%; Score 2956; DB 1; Length 579;
Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMAKAIKIALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMAKAIKIALSGK 60
QY 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSEFA 120
DB 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSEFA 120
QY 121 VVNVYSSKQARQALDKLNGFQLENFTLKVAATPDMAAQNPLQOPRGRGLGGRSS 180
DB 121 VVNVYSSKQARQALDKLNGFQLENFTLKVAATPDMAAQNPLQOPRGRGLGGRSS 180
QY 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKEGATIRNITKOTQSKIDVHRKEMAGA 240
DB 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKEGATIRNITKOTQSKIDVHRKEMAGA 240
QY 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFGRIGKEGRNLK 300
DB 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFGRIGKEGRNLK 300
QY 301 KIEDPDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRESEYENDIASMNL 360
DB 301 KIEDPDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNMLAGLFPPTSGMPPTSGPSPAMTPPYQFQSETEIYHOFPALSVGAI 420
DB 361 QAHLIPGLNMLAGLFPPTSGMPPTSGPSPAMTPPYQFQSETEIYHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASTIKIAPAPADAKVNMVITTPPEAOKFAKGRIGYKIEENFV 480
DB 421 IKGOGHIKOLSRFAGASTIKIAPAPADAKVNMVITTPPEAOKFAKGRIGYKIEENFV 480
QY 481 SKREEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVVPDQTPDENDQVVKIT 540
DB 481 SKREEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVVPDQTPDENDQVVKIT 540
QY 541 GHFYACOVAQRKIQELITLVOKHQOQKALQSGPPQSRK 579
DB 541 GHFYACOVAQRKIQELITLVOKHQOQKALQSGPPQSRK 579

RESULT 2
US-09-466-396A-176
; Sequence 176, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466, 396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-396A-176

Query Match
Best Local Similarity 100.0%; Score 2956; DB 18; Length 579;
Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMAKAIKIALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDPSMAKAIKIALSGK 60
QY 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSEFA 120
DB 61 IELHGKPIEVEHSVPRKORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSEFA 120
QY 121 VVNVYSSKQARQALDKLNGFQLENFTLKVAATPDMAAQNPLQOPRGRGLGGRSS 180
DB 121 VVNVYSSKQARQALDKLNGFQLENFTLKVAATPDMAAQNPLQOPRGRGLGGRSS 180
QY 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKEGATIRNITKOTQSKIDVHRKEMAGA 240
DB 181 RQSPGSVSKOKPCDPLRLVPTQFVGAIIKEGATIRNITKOTQSKIDVHRKEMAGA 240
QY 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFGRIGKEGRNLK 300
DB 241 EKSTILSTPEGTSAACKSILEIMHKEADIKFTEELPKILAHNNEFGRIGKEGRNLK 300
QY 301 KIEDPDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRESEYENDIASMNL 360
DB 301 KIEDPDTKITISPLQELTLNPERTIVKGNVETCAKAEEMKIRESEYENDIASMNL 360
QY 361 QAHLIPGLNMLAGLFPPTSGMPPTSGPSPAMTPPYQFQSETEIYHOFPALSVGAI 420
DB 361 QAHLIPGLNMLAGLFPPTSGMPPTSGPSPAMTPPYQFQSETEIYHOFPALSVGAI 420
QY 421 IKGOGHIKOLSRFAGASTIKIAPAPADAKVNMVITTPPEAOKFAKGRIGYKIEENFV 480
DB 421 IKGOGHIKOLSRFAGASTIKIAPAPADAKVNMVITTPPEAOKFAKGRIGYKIEENFV 480
QY 481 SKREEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVVPDQTPDENDQVVKIT 540
DB 481 SKREEVKLEAHIRVPSFAAGRVIGKGTVNEQLNLSAEVVPDQTPDENDQVVKIT 540
QY 541 GHFYACOVAQRKIQELITLVOKHQOQKALQSGPPQSRK 579
DB 541 GHFYACOVAQRKIQELITLVOKHQOQKALQSGPPQSRK 579

RESULT 3
US-09-476-496A-176
; Sequence 176, Application US/09476496A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476, 496A
; CURRENT FILING DATE: 1999-12-30.
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-496A-176

Query Match
Best Local Similarity 100.0%; Score 2956; DB 18; Length 579;
Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

QY 121 VVAVTSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
    |||
Db 121 VVAVTSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
QY 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240
    |||
Db 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240
QY 241 EKSTIIITSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
    |||
Db 241 EKSTIIITSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
QY 301 KIEDDDTKITISPLQELTLYNPERTITVKGNETCAKAEIEIMKKITRESEYNDIASMNL 360
    |||
Db 301 KIEDDDTKITISPLQELTLYNPERTITVKGNETCAKAEIEIMKKITRESEYNDIASMNL 360
QY 361 QAHILPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
    |||
Db 361 QAHILPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYITGPPEAOKAAGRITGKEENFY 480
    |||
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYITGPPEAOKAAGRITGKEENFY 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVELNQLSSAEVYVPRDQTPDENQVYVKIT 540
    |||
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVELNQLSSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACVQAORKIOEILITVYKHOQOKALQSGPPQSRK 579
    |||
Db 541 GHFYACVQAORKIOEILITVYKHOQOKALQSGPPQSRK 579

```

## RESULT 4.

```

US-09-480-884A-176
: Sequence 176, Application US/09480884A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45356
: CURRENT APPLICATION NUMBER: US/09/480, 884A
: CURRENT FILING DATE: 2001-08-27
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-480-884A-176

```

```

Query Match 100.0%; Score 2956; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNKLYIGNLSENAAPSDLESIFRDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
    |||
Db 1 MNKLYIGNLSENAAPSDLESIFRDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
QY 61 IELHGKPIEVEHVSVPKROIRIKLQIRNIPHLQMEVLDLSLVQGVYVSECOVNTDSETA 120
    |||
Db 61 IELHGKPIEVEHVSVPKROIRIKLQIRNIPHLQMEVLDLSLVQGVYVSECOVNTDSETA 120
QY 121 VVAVTSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
    |||
Db 121 VVAVTSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
QY 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240
    |||
Db 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240

```

```

Db 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240
    |||
QY 241 EKSTIIITSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
    |||
Db 241 EKSTIIITSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
QY 301 KIEDDDTKITISPLQELTLYNPERTITVKGNETCAKAEIEIMKKITRESEYNDIASMNL 360
    |||
Db 301 KIEDDDTKITISPLQELTLYNPERTITVKGNETCAKAEIEIMKKITRESEYNDIASMNL 360
QY 361 QAHILPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
    |||
Db 361 QAHILPGLNINLALGFPPTSGMPPTSGPPSAMTPPYQFQSETEVHOFIPALSVGAI 420
QY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYITGPPEAOKAAGRITGKEENFY 480
    |||
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYITGPPEAOKAAGRITGKEENFY 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVELNQLSSAEVYVPRDQTPDENQVYVKIT 540
    |||
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVELNQLSSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACVQAORKIOEILITVYKHOQOKALQSGPPQSRK 579
    |||
Db 541 GHFYACVQAORKIOEILITVYKHOQOKALQSGPPQSRK 579

```

## RESULT 5

```

US-09-510-376A-176
: Sequence 176, Application US/09510376A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45567
: CURRENT APPLICATION NUMBER: US/09/510, 376A
: CURRENT FILING DATE: 2001-08-21
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-510-376A-176

```

```

Query Match 100.0%; Score 2956; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNKLYIGNLSENAAPSDLESIFRDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
    |||
Db 1 MNKLYIGNLSENAAPSDLESIFRDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIKIALSGK 60
QY 61 IELHGKPIEVEHVSVPKROIRIKLQIRNIPHLQMEVLDLSLVQGVYVSECOVNTDSETA 120
    |||
Db 61 IELHGKPIEVEHVSVPKROIRIKLQIRNIPHLQMEVLDLSLVQGVYVSECOVNTDSETA 120
QY 121 VVAVTSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
    |||
Db 121 VVAVTSSKQDARQALDKLNGFQLENTLKVAYIPDEMAAQNPLQOPRGRLGQGRSS 180
QY 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240
    |||
Db 181 ROSPGSVSKOKPCDPLRLVLPVTOFGVAILGKEGATIRNITKOTOSKIDVHKRENAGAA 240
QY 241 EKSTIIITSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300
    |||
Db 241 EKSTIIITSTPEGSTSAACKSILEIMHKEADIKFTEIEIPKLILANNVGRILGEGRNK 300

```

```
OY 301 KIEODDTKTTISPLQELTLYNPERTIVKGNVETCKAAEEMKIKRESYENDIASNL 360
DB 301 KIEODDTKTTISPLQELTLYNPERTIVKGNVETCKAAEEMKIKRESYENDIASNL 360
OY 361 QAHILPGNLNMLGLFPPTSGMPPTSGPSPAMPPEPOFPOSEETVHOFPALSVGI 420
DB 361 QAHILPGNLNMLGLFPPTSGMPPTSGPSPAMPPEPOFPOSEETVHOFPALSVGI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
OY 481 SPEEVEKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPRDQTPDENDDVYVKIT 540
DB 481 SPEEVEKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPRDQTPDENDDVYVKIT 540
OY 541 GHFYACQVAKRKIOELITLVOKHOQOKALOSGPQSRK 579
DB 541 GHFYACQVAKRKIOELITLVOKHOQOKALOSGPQSRK 579

RESULT 6
US-09-542-615A-176
Sequence 176, Application US/09542615A
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Katos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasar A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542.615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PR
ORGANISM: Homo sapiens
US-09-542-615A-176

Query Match 100.0%; Score 2956; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
OY 61 IELHGKPIEVEHVSVPKROIRKLOIRNIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
DB 61 IELHGKPIEVEHVSVPKROIRKLOIRNIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
OY 121 VVNVYSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQQNPLOQPRGRGLGGRGSS 180
DB 121 VVNVYSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQQNPLOQPRGRGLGGRGSS 180
OY 181 RQSPGSVSKQPCDPLRLVLPQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKQPCDPLRLVLPQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
OY 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEBIPKTLIAHNNVGRILGEGRNK 300
DB 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEBIPKTLIAHNNVGRILGEGRNK 300
OY 301 KIEODDTKTTISPLQELTLYNPERTIVKGNVETCKAAEEMKIKRESYENDIASNL 360
DB 301 KIEODDTKTTISPLQELTLYNPERTIVKGNVETCKAAEEMKIKRESYENDIASNL 360
```

```
OY 361 QAHILPGNLNMLGLFPPTSGMPPTSGPSPAMPPEPOFPOSEETVHOFPALSVGI 420
DB 361 QAHILPGNLNMLGLFPPTSGMPPTSGPSPAMPPEPOFPOSEETVHOFPALSVGI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKVRVYITGPEAOFKAOGRIYKIKEENFV 480
OY 481 SPEEVEKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPRDQTPDENDDVYVKIT 540
DB 481 SPEEVEKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPRDQTPDENDDVYVKIT 540
OY 541 GHFYACQVAKRKIOELITLVOKHOQOKALOSGPQSRK 579
DB 541 GHFYACQVAKRKIOELITLVOKHOQOKALOSGPQSRK 579

RESULT 7
US-09-606-421A-176
Sequence 176, Application US/09606421A
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Katos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasar A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/606.421A
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 354
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PR
ORGANISM: Homo sapiens
US-09-606-421A-176

Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60
OY 61 IELHGKPIEVEHVSVPKROIRKLOIRNIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
DB 61 IELHGKPIEVEHVSVPKROIRKLOIRNIPHLQMEVLDLSLVOYGVESCEQVNTDSETA 120
OY 121 VVNVYSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQQNPLOQPRGRGLGGRGSS 180
DB 121 VVNVYSSKDAQALDKLNGFOLNFTLKAVYIPDEMAAQQNPLOQPRGRGLGGRGSS 180
OY 181 RQSPGSVSKQPCDPLRLVLPQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 RQSPGSVSKQPCDPLRLVLPQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
OY 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEBIPKTLIAHNNVGRILGEGRNK 300
DB 241 EKSTILLSTPEGSTAACKSILEIMHKEADIKFTEBIPKTLIAHNNVGRILGEGRNK 300
OY 301 KIEODDTKTTISPLQELTLYNPERTIVKGNVETCKAAEEMKIKRESYENDIASNL 360
DB 301 KIEODDTKTTISPLQELTLYNPERTIVKGNVETCKAAEEMKIKRESYENDIASNL 360
OY 361 QAHILPGNLNMLGLFPPTSGMPPTSGPSPAMPPEPOFPOSEETVHOFPALSVGI 420
DB 361 QAHILPGNLNMLGLFPPTSGMPPTSGPSPAMPPEPOFPOSEETVHOFPALSVGI 420
```

Db 361 QAHILPGLNLTALGLPPTSGMPPTSGPSAMTPPYPOFEOSETETVHOFTALSVGAI 420  
OY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPEAOFKAQGRITGIKEENFV 480  
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPEAOFKAQGRITGIKEENFV 480  
OY 481 SPKEEVLEHIVPSPFAGRVIGKGGKTVNELONLSSAEVVPDQYPTDENDQVYVKIT 540  
Db 481 SPKEEVLEHIVPSPFAGRVIGKGGKTVNELONLSSAEVVPDQYPTDENDQVYVKIT 540  
OY 541 GHFYACQVAORRKOIEILLTVKOHQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORRKOIEILLTVKOHQOKALQSGPPQSRK 579

## RESULT 8

US-09-606-421B-176  
Sequence 176, Application US/09606421B  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421B  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-606-421B-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 8,6e-243; Indels 0; Gaps 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGK 60  
OY 61 TELHGRLEVEHSPKQRIRKIQIRNIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
Db 61 TELHGRLEVEHSPKQRIRKIQIRNIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
OY 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAYIPDEMAQONPLQOPRGRGLGGRSS 180  
Db 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAYIPDEMAQONPLQOPRGRGLGGRSS 180  
OY 181 RQSGSGSVSKQKQDPLRLVLPQFVGAIIGEGATIRNITKQOSKIDVHKENAGAA 240  
Db 181 RQSGSGSVSKQKQDPLRLVLPQFVGAIIGEGATIRNITKQOSKIDVHKENAGAA 240  
OY 241 EKSTITLSTPEGTSAAKSIILEIMHKEADIKFTEERIPKLITLAHNNFVGRILGKGRNLK 300  
Db 241 EKSTITLSTPEGTSAAKSIILEIMHKEADIKFTEERIPKLITLAHNNFVGRILGKGRNLK 300  
OY 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETAKAEELIMKIRRESYENDIASMNL 360  
Db 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETAKAEELIMKIRRESYENDIASMNL 360  
OY 361 QAHILPGLNLTALGLPPTSGMPPTSGPSAMTPPYPOFEOSETETVHOFTALSVGAI 420  
Db 361 QAHILPGLNLTALGLPPTSGMPPTSGPSAMTPPYPOFEOSETETVHOFTALSVGAI 420

OY 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPEAOFKAQGRITGIKEENFV 480  
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMVITITGPPEAOFKAQGRITGIKEENFV 480  
OY 481 SPKEEVLEHIVPSPFAGRVIGKGGKTVNELONLSSAEVVPDQYPTDENDQVYVKIT 540  
Db 481 SPKEEVLEHIVPSPFAGRVIGKGGKTVNELONLSSAEVVPDQYPTDENDQVYVKIT 540  
OY 541 GHFYACQVAORRKOIEILLTVKOHQOKALQSGPPQSRK 579  
Db 541 GHFYACQVAORRKOIEILLTVKOHQOKALQSGPPQSRK 579

## RESULT 9

US-09-630-940A-176  
Sequence 176, Application US/09630940A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C10  
CURRENT APPLICATION NUMBER: US/09/630,940A  
NUMBER OF SEQ ID NOS: 367  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-630-940A-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 8,6e-243; Indels 0; Gaps 0;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSGK 60  
OY 61 TELHGRLEVEHSPKQRIRKIQIRNIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
Db 61 TELHGRLEVEHSPKQRIRKIQIRNIPHLQMEVLDLVOYGVESECEVNTDSETA 120  
OY 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAYIPDEMAQONPLQOPRGRGLGGRSS 180  
Db 121 VVNTYSSKQDARQALDKLNGFQLENFTLKVAYIPDEMAQONPLQOPRGRGLGGRSS 180  
OY 181 RQSGSGSVSKQKQDPLRLVLPQFVGAIIGEGATIRNITKQOSKIDVHKENAGAA 240  
Db 181 RQSGSGSVSKQKQDPLRLVLPQFVGAIIGEGATIRNITKQOSKIDVHKENAGAA 240  
OY 241 EKSTITLSTPEGTSAAKSIILEIMHKEADIKFTEERIPKLITLAHNNFVGRILGKGRNLK 300  
Db 241 EKSTITLSTPEGTSAAKSIILEIMHKEADIKFTEERIPKLITLAHNNFVGRILGKGRNLK 300  
OY 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETAKAEELIMKIRRESYENDIASMNL 360  
Db 301 KIEODTDTKITISPLQELTLYNPERITTVKGNVETAKAEELIMKIRRESYENDIASMNL 360  
OY 361 QAHILPGLNLTALGLPPTSGMPPTSGPSAMTPPYPOFEOSETETVHOFTALSVGAI 420  
Db 361 QAHILPGLNLTALGLPPTSGMPPTSGPSAMTPPYPOFEOSETETVHOFTALSVGAI 420

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Qy	481	SKPEVKLKAHINVP	FAAGRVYKGGKTYNELON	SSAEVYVRRDTP	PENDVYVYIT	540
Db	481	SKPEVKLKAHINVP	FAAGRVYKGGKTYNELON	SSAEVYVRRDTP	PENDVYVYIT	540
Qy	541	GHEFYACQYAAQRK	TDLELLDYKADQQAALASG	PPGSRKK		579
Db	541	GHEFYACQYAAQRK	TDLELLDYKADQQAALASG	PPGSRKK		579

```

RESULT 10
US-09-630-940B-176
; Sequence 176, Application US/09630940B
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45C10
CURRENT APPLICATION NUMBER: US/09/630.940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ. ID NOS: 367
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRF
ORGANISM: Homo sapiens
US-09-630-940B-176

```

[illegible]

Qy	421	IKQOQOHIKOISRPAAASIKIPAEADADAVRWVITITPPEADQKQGIYKIKIEENFV	480
Dd	421	IKQOQHITKOLSTRPAASAKIIPAEADADAVRWVITITPPEADQKQGIYKIKIEENFV	480
Qy	481	SKKEEVKTEAHINVPFAAGRVITKGGKTYNELONLSAEVNVPRQPTDENDQVYVKIT	540
Dd	481	SKKEEVKTEAHINVPFAAGRVITKGGKTYNELONLSAEVNVPRQPTDENDQVYVKIT	540
Qy	541	GHPYACQYAOARKIDELLIVYKHOQKAAALOSPPQSRK	579
Dd	541	GHPYACQYAOARKIDELLIVYKHOQKAAALOSPPQSRK	579

```

RESULT 11
US-09-662-786-176
Sequence 176, Application US/09662786
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasser A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE REFERENCE: 210121.455C12
FILE REFERENCE: 210121.455C12
CURRENT APPLICATION NUMBER: US/09/662,786
CURRENT FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-662-786-176

```

Query Match	Similarity	100.0%	Score	2956	DB	20	Length	579
Best Local	Similarity	100.0% <td>Pred. No.</td> <td>8.6e+243</td> <td></td> <td></td> <td></td> <td></td>	Pred. No.	8.6e+243				
Matches	579	Conservative	0	Mismatches	0	Indels	0	Gaps
QY	1	MNLTYGNLSNMAPSDLESIFPKADKIPVSGCFVLTGKGAFAVCCPDPSWALKATIEALSGK	60					
Db	1	MNLTYGNLSNMAPSDLESIFPKADKIPVSGCFVLTGKGAFAVCCPDPSWALKATIEALSGK	60					
QY	61	IELHGKPIEVEHSVAPKRRQRIKQIKNIPHLMQEVDSLVLVQGVESCEQVNDSETA	120					
Db	61	IELHGKPIEVEHSVAPKRRQRIKQIKNIPHLMQEVDSLVLVQGVESCEQVNDSETA	120					
QY	121	VVVVYSSKDDARALDLKNGPQLENTLTKAAYIPDEMAAQQPPLDQPPGRGSGGSSS	180					
Db	121	VVVVYSSKDDARALDLKNGPQLENTLTKAAYIPDEMAAQQPPLDQPPGRGSGGSSS	180					
QY	181	ROSPPSSVSKKPCDPLRLVLTPTQVGAIIIGKSGATIRNITKQTSKIDYHREKNGAA	240					
Db	181	ROSPPSSVSKKPCDPLRLVLTPTQVGAIIIGKSGATIRNITKQTSKIDYHREKNGAA	240					
QY	241	EKSITILSPGSTNAACKSTLEITMKHEQODIKFEEELPKILLAHNNFVRLIGKGNLK	300					
Db	241	EKSITILSPGSTNAACKSTLEITMKHEQODIKFEEELPKILLAHNNFVRLIGKGNLK	300					
QY	301	KIKQDIDPKIKTISPLQDELTYNPEERTYVKGVEFLCAAEELTMKIRPSYNDIASNML	360					
Db	301	KIKQDIDPKIKTISPLQDELTYNPEERTYVKGVEFLCAAEELTMKIRPSYNDIASNML	360					
QY	361	QAHLIPGLNALNGLPPTSGMPPPISGPPSAMPPIYPOEBOSETTYVQIFPALSGAI	420					
Db	361	QAHLIPGLNALNGLPPTSGMPPPISGPPSAMPPIYPOEBOSETTYVQIFPALSGAI	420					

OY	421	IGKGOHITKOLSRFAGS	SIKPAEADADAVRWIT	INGPEAOFKKOGRIYKIKRENV	48
		IGKGOHITKOLSRFAGS	SIKPAEADADAVRWIT	INGPEAOFKKOGRIYKIKRENV	48
Db	421	IGKGOHITKOLSRFAGS	SIKPAEADADAVRWIT	INGPEAOFKKOGRIYKIKRENV	480
OY	481	SPKEEVKLEAHIRVPSRAGV	IGKGTYNELONSSA	VVPVPROTPENDNOVVKIT	540
		SPKEEVKLEAHIRVPSRAGV	IGKGTYNELONSSA	VVPVPROTPENDNOVVKIT	540
Db	481	SPKEEVKLEAHIRVPSRAGV	IGKGTYNELONSSA	VVPVPROTPENDNOVVKIT	540
OY	541	GHEFYACVOAKRKIOELL	TOVKOHOOAKALSG	PPOSHRK	579
		GHEFYACVOAKRKIOELL	TOVKOHOOAKALSG	PPOSHRK	579
Db	541	GHEFYACVOAKRKIOELL	TOVKOHOOAKALSG	PPOSHRK	579

```

RESULT 12
US-09-685-696-176
: Sequence 176, Application US/09685696
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yashir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C13
CURRENT APPLICATION NUMBER: US/09/685,696
CURRENT FILING DATE: 2000-10-09
NUMBER OF SEQ. ID NOS.: 381
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-685-696-176

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Query Match	100.0%	Score 2956	DB 20	Length 579
Best Local Similarity	100.0%	Pred. No. 8.6e-243		
Matches 579	Conservative	0	Mismatches 0	Indels 0
				Gaps 0
QY 1	MNKLIIIGNLSEMAPSDLESIFRDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60			
Db 1	MNKLIIIGNLSEMAPSDLESIFRDAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60			
QY 61	IELHGKRIEVEHSPVKRRIKRIKQIRNIIPPHIQMEVLDLSLVGYGVSESCQVNTDSE7A 120			
Db 61	IELHGKRIEVEHSPVKRRIKRIKQIRNIIPPHIQMEVLDLSLVGYGVSESCQVNTDSE7A 120			
QY 121	VVNVNTYSSKQAOALDKLNGFOLNFETLKVAYIPDEMAAONPILPOORGRGRIGLGOGSS 180			
Db 121	VVNVNTYSSKQAOALDKLNGFOLNFETLKVAYIPDEMAAONPILPOORGRGRIGLGOGSS 180			
QY 181	ROGSPGVSVKORPCDLPRLVLVPTQVGAIIIGKEGATIRNTKOTOSKIDVYHREKNAA 240			
Db 181	ROGSPGVSVKORPCDLPRLVLVPTQVGAIIIGKEGATIRNTKOTOSKIDVYHREKNAA 240			
QY 241	EKSTIIISTPEGVSACKSIIETIMKHEADIKFTEIEIPLKLIANNPVGRLIGKEGNLK 300			
Db 241	EKSTIIISTPEGVSACKSIIETIMKHEADIKFTEIEIPLKLIANNPVGRLIGKEGNLK 300			
QY 301	KIEODDTTKITTIIPLOELTYNPERTIYKGVWEFCAKAEIEIMKKITRESEYNDIASMNL 360			
Db 301	KIEODDTTKITTIIPLOELTYNPERTIYKGVWEFCAKAEIEIMKKITRESEYNDIASMNL 360			
QY 361	QAHILPELINALGLFPPTSGMPPTSGPPSAMPPYQFQDSQETEVHOFIPALSVGAT 420			
Db 361	QAHILPELINALGLFPPTSGMPPTSGPPSAMPPYQFQDSQETEVHOFIPALSVGAT 420			

QY	421	IKGOGHIOKLSFASASIKTAPAEADPAVRYWITITGPEOFOAGRIYGIKIKENFV	4800
Db	421	IGMOGHIKLSFASASIKTAPAEADPAVRYWITITGPEOFOAGRIYGIKIKENFV	4800
QY	421	IKGOGHIOKLSFASASIKTAPAEADPAVRYWITITGPEOFOAGRIYGIKIKENFV	4800
Db	421	IGMOGHIKLSFASASIKTAPAEADPAVRYWITITGPEOFOAGRIYGIKIKENFV	4800
QY	481	SPKEEVKLEAHIRVSPFAAGRTIGKGTATVNEONLSAENVVPRQTPDEMDQVYVIT	5400
Db	481	SPKEEVKLEAHIRVSPFAAGRTIGKGTATVNEONLSAENVVPRQTPDEMDQVYVIT	5400
QY	541	GHEFYACQVAORIKTOETITRVKOHQOKALSGPPQSRK	579
Db	541	GHEFYACQVAORIKTOETITRVKOHQOKALSGPPQSRK	579

```

: RESULT 13
: US-09-735-705-176
: Sequence 176, Application US/09735705
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Nell
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-735-705-176

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Query Match	100.0%	Score 2956	DB 21	Length 579
Best Local Similarity	100.0%	Pred. No. 8.6e-243		
Matches 579	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	MNKLTYGNLSMNA	PSDLSIEFKDAKIPVSGPFLVKTGYAFVDCDPDSESMALKAIEALSG	60	
DB 1	MNKLTYGNLSMNA	PSDLSIEFKDAKIPVSGPFLVKTGYAFVDCDPDSESMALKAIEALSG	60	
QY 61	IELGKPELEVESHYPRKORIRKIQIRNIPRHQMEVLDLSLVQYGVSECEVNTBSEFA	120		
DB 61	IELGKPELEVESHYPRKORIRKIQIRNIPRHQMEVLDLSLVQYGVSECEVNTBSEFA	120		
QY 121	VVNTYSSKQARQALDLKNGFQLENFTLKVAVIPDEMAAQNPLQDPGRGRIGQGRSS	180		
DB 121	VVNTYSSKQARQALDLKNGFQLENFTLKVAVIPDEMAAQNPLQDPGRGRIGQGRSS	180		
QY 181	ROGSPGVSYSKQPCDDPLRLVPTQFVGAIIGKEGATIRNITKQTSKIDVHKRENAGAA	240		
DB 181	ROGSPGVSYSKQPCDDPLRLVPTQFVGAIIGKEGATIRNITKQTSKIDVHKRENAGAA	240		
QY 241	EKSTIIISTPEGYSAAKCSILETMMHEADQIKFTEBIRPLKILAHNNVYGRIGKEGNLK	300		
DB 241	EKSTIIISTPEGYSAAKCSILETMMHEADQIKFTEBIRPLKILAHNNVYGRIGKEGNLK	300		
QY 301	KIEODDTKRTITISHLQELTYLNPERRITVKGAVETCAKAEIEIMKKITRESYENDIASMNL	360		
DB 301	KIEODDTKRTITISHLQELTYLNPERRITVKGAVETCAKAEIEIMKKITRESYENDIASMNL	360		
QY 361	QAHILPGLNMLALGLPPTSGMPPPSGPPSMTPTPTQFQDSETEVYHOFITALSYGAI	420		
DB 361	QAHILPGLNMLALGLPPTSGMPPPSGPPSMTPTPTQFQDSETEVYHOFITALSYGAI	420		



Db 481 SPKEVYVLEAHIRVPSFAGRVIGKGGKTVNELNLSSAEVVPDDOTPDENDQVYVKIT 540  
OY 541 GHFYACVVAQRKIOEILTQVKOHOOOKALQSGPPQSRRK 579  
Db 541 GHFYACVVAQRKIOEILTQVKOHOOOKALQSGPPQSRRK 579

Search completed: April 16, 2003, 16:29:56  
Job time : 390.852 secs





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Page 1

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:21:35 ; Search time 43.734 Seconds

(without alignments)  
1001.062 Million cell updates/sec

Title: US-09-897-778-176

Perfect score: 2956

Sequence: 1 MNKLYIGLSENAFSDLES.....VKHQOQKALQSGPFSNRK 579

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:\*\*

1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2956	100.0	579	10	US-09-735-705-176 Sequence 176, App
2	2956	100.0	579	10	US-09-850-716A-176 Sequence 176, App
3	2956	100.0	579	10	US-09-897-778-176 Sequence 176, App
4	2943	99.6	579	10	US-09-735-705-176 Sequence 348, App
5	2943	99.6	579	10	US-09-850-716A-348 Sequence 348, App
6	2943	99.6	579	10	US-09-897-778-348 Sequence 348, App
7	2943	99.6	579	10	US-09-897-778-446 Sequence 446, App
8	2943	99.6	579	10	US-09-897-778-449 Sequence 446, App
9	2938	99.4	586	10	US-09-850-716A-427 Sequence 427, App
10	2938	99.4	586	10	US-09-850-716A-427 Sequence 427, App
11	2190	74.1	577	10	US-09-897-778-427 Sequence 2, Appl
12	1946.5	65.8	620	10	US-09-764-864-1116 Sequence 1116, Ap
13	949	32.1	261	10	US-09-764-864-1114 Sequence 1114, Ap
14	919	31.1	250	10	US-09-764-864-1132 Sequence 1132, Ap
15	636	21.2	171	10	US-09-764-864-1119 Sequence 1119, Ap
16	527	17.8	192	10	US-09-764-864-1117 Sequence 1117, Ap
17	474	16.0	93	10	US-09-864-761-48606 Sequence 48606, A
18	402	13.6	171	10	US-09-764-864-1536 Sequence 1536, A
19	238	8.1	49	10	US-09-873-637-22 Sequence 22, Appl

#### ALIGNMENTS

20	237	8.0	48	10	US-09-873-637-24	Sequence 24, Appl
21	232	7.8	49	10	US-09-873-637-18	Sequence 18, Appl
22	227	7.7	45	10	US-09-864-761-45587	Sequence 45587, A
23	227	7.7	47	10	US-09-873-637-23	Sequence 23, Appl
24	225	7.6	47	10	US-09-873-637-21	Sequence 21, Appl
25	219	7.4	48	10	US-09-873-637-20	Sequence 20, Appl
26	218	7.4	47	10	US-09-873-637-17	Sequence 17, Appl
27	190	6.4	47	10	US-09-873-637-19	Sequence 19, Appl
28	187	6.3	46	10	US-09-925-301-1198	Sequence 1198, Ap
29	171	5.8	47	10	US-09-764-864-1534	Sequence 1534, Ap
30	141	4.8	39	9	US-10-025-367-25	Sequence 25, Appl
31	139.5	4.7	1179	9	US-09-821-883-29	Sequence 29, Appl
32	135.5	4.6	359	9	US-10-025-367-23	Sequence 23, Appl
33	134.5	4.6	337	9	US-10-102-806-570	Sequence 570, App
34	133	4.5	380	9	US-10-025-367-27	Sequence 27, Appl
35	132	4.5	201	10	US-09-764-864-1113	Sequence 1113, Ap
36	131.5	4.4	279	12	US-10-014-927-19	Sequence 19, Appl
37	130	4.4	633	10	US-09-821-687-10	Sequence 10, Appl
38	129.5	4.4	545	10	US-09-978-242-1	Sequence 1, Appl
39	128.5	4.4	579	10	US-09-925-300-1415	Sequence 1415, Ap
40	128.5	4.3	561	10	US-09-821-687-4	Sequence 4, Appl
41	125.5	4.2	1601	10	US-09-925-300-1620	Sequence 1620, Ap
42	124	4.2	1601	10	US-09-862-027-40	Sequence 40, Appl
43	123.5	4.1	366	9	US-10-029-180-66	Sequence 66, Appl
44	121.5	4.1	915	9	US-10-029-180-74	Sequence 74, Appl
45	120	4.1	261	9	US-10-043-487-220	Sequence 220, Appl

RESULT 1  
US-09-735-705-176  
Sequence 176, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-176

Query Match 100.0%; Score 2956; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 9,7e-218;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGLSENAFSDLESIFKDKATIPVSGPIVKTGYAFVDCPDSESMALKATEALISGK 60  
DB 1 MNKLYIGLSENAFSDLESIFKDKATIPVSGPIVKTGYAFVDCPDSESMALKATEALISGK 60  
QY 61 IELHGRPIEVHSPKRRIRKQIRNIPPHLQWELVDSLVQYGVVSCDQVNTDSETA 120  
DB 61 IELHGRPIEVHSPKRRIRKQIRNIPPHLQWELVDSLVQYGVVSCDQVNTDSETA 120

```

OY 121 VVNVYSSKDOARQALDKLNGFOLNENFTLKAVIPDEMAAQNLOOPRGRGLGORGSS 180
    |||||||
DB 121 VVNVYSSKDOARQALDKLNGFOLNENFTLKAVIPDEMAAQNLOOPRGRGLGORGSS 180
OY 181 ROGSPGSVSKOKPCDPLRLVLPVTOFGALIGKBEATIRNTKTQOSKIDVHRKENAGAA 240
    |||||||
DB 181 ROGSPGSVSKOKPCDPLRLVLPVTOFGALIGKBEATIRNTKTQOSKIDVHRKENAGAA 240
OY 241 EKSTILSTPEGTSAAKSLIETIMHKAODIKFTEIPLKILANNVGLIGKGRNLIK 300
    |||||||
DB 241 EKSTILSTPEGTSAAKSLIETIMHKAODIKFTEIPLKILANNVGLIGKGRNLIK 300
OY 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETICAKAEIEIMKIRESEYENDIASNML 360
    |||||||
DB 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETICAKAEIEIMKIRESEYENDIASNML 360
OY 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSANTPPYPOFQOSETETVHOFPALSVGAI 420
    |||||||
DB 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSANTPPYPOFQOSETETVHOFPALSVGAI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMIITGPPEAQKAGRIYGIKEENFV 480
    |||||||
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMIITGPPEAQKAGRIYGIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPVPRDQTPDENOVVVKIT 540
    |||||||
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPVPRDQTPDENOVVVKIT 540
OY 541 GHFYACQVAORKIOELITOVKHOQOKALOGSPPOSRRK 579
    |||||||
DB 541 GHFYACQVAORKIOELITOVKHOQOKALOGSPPOSRRK 579

RESULT 2
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US2002015139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match 100.0%; Score 2956; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,7e-218;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 241 EKSTILSTPEGTSAAKSLIETIMHKAODIKFTEIPLKILANNVGLIGKGRNLIK 300
    |||||||
DB 241 EKSTILSTPEGTSAAKSLIETIMHKAODIKFTEIPLKILANNVGLIGKGRNLIK 300
OY 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETICAKAEIEIMKIRESEYENDIASNML 360
    |||||||
DB 301 KIEODPTKTIISPLQELTLYNPERTITVGNVETICAKAEIEIMKIRESEYENDIASNML 360
OY 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSANTPPYPOFQOSETETVHOFPALSVGAI 420
    |||||||
DB 361 QAHILPGLNMLAGLFPPTSGMPPTSGPSANTPPYPOFQOSETETVHOFPALSVGAI 420
OY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMIITGPPEAQKAGRIYGIKEENFV 480
    |||||||
DB 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMIITGPPEAQKAGRIYGIKEENFV 480
OY 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPVPRDQTPDENOVVVKIT 540
    |||||||
DB 481 SPKEEVKLEAHIRVPSFAGRVIGKGTVNELONLSSAEVVPVPRDQTPDENOVVVKIT 540
OY 541 GHFYACQVAORKIOELITOVKHOQOKALOGSPPOSRRK 579
    |||||||
DB 541 GHFYACQVAORKIOELITOVKHOQOKALOGSPPOSRRK 579

RESULT 3
US-09-897-778-176
: Sequence 176, Application US/09897778
: Patent No. US2002014713A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-176

Query Match 100.0%; Score 2956; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,7e-218;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLIGKEGRNK 300
DB 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLIGKEGRNK 300
QY 301 KIEODTDTKRTITISPLQELTYLNPERTITVKGAVETCAKAEELIMKKITRESEYENDIASMNL 360
DB 301 KIEODTDTKRTITISPLQELTYLNPERTITVKGAVETCAKAEELIMKKITRESEYENDIASMNL 360
QY 361 QAHILPGNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQOSETEVTHOIFALSVGAI 420
DB 361 QAHILPGNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQOSETEVTHOIFALSVGAI 420
QY 421 IKGOGOHKOLSRPAGASIKIAPAEAPDAKVMVITITGPPPAOKRAGRIYGIKEENY 480
DB 421 IKGOGOHKOLSRPAGASIKIAPAEAPDAKVMVITITGPPPAOKRAGRIYGIKEENY 480
QY 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACQVAKRKIOEILTYQKHOQOKALQSGPPSRRK 579
DB 541 GHFYACQVAKRKIOEILTYQKHOQOKALQSGPPSRRK 579

```

## RESULT 4

```

US-09-735-705-348
Sequence 348, Application US/09735705
Patent No. US200200522929A1
GENERAL INFORMATION:
APPLICANT: Wang, Honglong
APPLICANT: Fan, Liguang
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-348

```

```

Query Match 99.6%; Score 2943; DB 10; Length 579;
Best Local Similarity 99.7%; Pred. No. 9,6e-217;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
QY 61 IELHCKPIEVESHVPRKQRIKIQIRNIPPHLOMEVLDLSLVQGVVSCQOVNTDSETA 120
DB 61 IELHCKPIEVESHVPRKQRIKIQIRNIPPHLOMEVLDLSLVQGVVSCQOVNTDSETA 120
QY 121 VVNVTVSSKDDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRRIGLGGSS 180
DB 121 VVNVTVSSKDDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRRIGLGGSS 180
QY 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240

```

```

DB 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLIGKEGRNK 300
DB 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLIGKEGRNK 300
QY 301 KIEODTDTKRTITISPLQELTYLNPERTITVKGAVETCAKAEELIMKKITRESEYENDIASMNL 360
DB 301 KIEODTDTKRTITISPLQELTYLNPERTITVKGAVETCAKAEELIMKKITRESEYENDIASMNL 360
QY 361 QAHILPGNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQOSETEVTHOIFALSVGAI 420
DB 361 QAHILPGNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQOSETEVTHOIFALSVGAI 420
QY 421 IKGOGOHKOLSRPAGASIKIAPAEAPDAKVMVITITGPPPAOKRAGRIYGIKEENY 480
DB 421 IKGOGOHKOLSRPAGASIKIAPAEAPDAKVMVITITGPPPAOKRAGRIYGIKEENY 480
QY 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDQTPDENQVYVKIT 540
DB 481 SPKEEVKLEAHIRVSPFAAGRVIGKGGKTVNELONLSAEVYVPRDQTPDENQVYVKIT 540
QY 541 GHFYACQVAKRKIOEILTYQKHOQOKALQSGPPSRRK 579
DB 541 GHFYACQVAKRKIOEILTYQKHOQOKALQSGPPSRRK 579

```

## RESULT 5

```

US-09-850-716A-348
Sequence 348, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-348

```

```

Query Match 99.6%; Score 2943; DB 10; Length 579;
Best Local Similarity 99.7%; Pred. No. 9,6e-217;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFDKAKIPVSGPLVKTGYAFVDDPDSMALKALAEALSGK 60
QY 61 IELHCKPIEVESHVPRKQRIKIQIRNIPPHLOMEVLDLSLVQGVVSCQOVNTDSETA 120
DB 61 IELHCKPIEVESHVPRKQRIKIQIRNIPPHLOMEVLDLSLVQGVVSCQOVNTDSETA 120
QY 121 VVNVTVSSKDDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRRIGLGGSS 180
DB 121 VVNVTVSSKDDARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRRIGLGGSS 180
QY 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
DB 181 RQSGSGSVSKOPCDLPLRLVPTQFVGAILKEGATIRNITKQTSKIDVHRKENAGAA 240
QY 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLIGKEGRNK 300
DB 241 EKSTITLSTPGTSAACKSILEIMHKEADIKFTEETPLKTLAHNNFVGLIGKEGRNK 300
QY 301 KIEODTDTKRTITISPLQELTYLNPERTITVKGAVETCAKAEELIMKKITRESEYENDIASMNL 360
DB 301 KIEODTDTKRTITISPLQELTYLNPERTITVKGAVETCAKAEELIMKKITRESEYENDIASMNL 360

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Thu Apr 17 07:55:18 2003

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Page 4

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Db 301 KIEODTRKTIISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Oy 361 QAHILIPGLNALGLFPPTSGMPPTSGPSPAMTPPYPOFOSSETETVHOFIPALSVGAI 420
Db 361 QAHILIPGLNALGLFPPTSGMPPTSGPSPAMTPPYPOFOSSETETVHOFIPALSVGAI 420
Oy 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAQFAAGRTIGKIREENV 480
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAQFAAGRTIGKIREENV 480
Oy 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Db 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Oy 541 GHFYACOVAORKIOELITVYKHOQOKALOGSPQSRK 579
Db 541 GHFYACOVAORKIOELITVYKHOQOKALOGSPQSRK 579
```

RESULT 6

```
US-09-897-778-348
: Sequence 348, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897.778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ NOS: 467
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-897-778-348
```

Query Match 99.6% Score 2943: DB 10: Length 579:  
Best Local Similarity 99.7% Pred. No. 9.6e-217:  
Matches 577: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

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Oy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTKGYAFVDCPDSEMAKAIEMALSG 60
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTKGYAFVDCPDSEMAKAIEMALSG 60
Oy 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPRLQEWYLDLSLOYGVVSCQVNTDSEFA 120
Db 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPRLQEWYLDLSLOYGVVSCQVNTDSEFA 120
Oy 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Db 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Oy 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAIGKAGATIRNITKQOSKIDVHREKENGAA 240
Db 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAIGKAGATIRNITKQOSKIDVHREKENGAA 240
Oy 241 EKSTITLSTPEGTSAACKSILEIMKEADIKFTEELPKLIHNNFVGRIGEGRNK 300
Db 241 EKSTITLSTPEGTSAACKSILEIMKEADIKFTEELPKLIHNNFVGRIGEGRNK 300
Oy 301 KIEODTRKTIISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Db 301 KIEODTRKTIISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
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Db 301 KIEODTRKTIISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Oy 361 QAHILIPGLNALGLFPPTSGMPPTSGPSPAMTPPYPOFOSSETETVHOFIPALSVGAI 420
Db 361 QAHILIPGLNALGLFPPTSGMPPTSGPSPAMTPPYPOFOSSETETVHOFIPALSVGAI 420
Oy 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAQFAAGRTIGKIREENV 480
Db 421 IKGOGHITKOLSRFAGASIKIAPAEAPDAKVMYIITGPPEAQFAAGRTIGKIREENV 480
Oy 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Db 481 SPEEYKLEAHIRVPSFAGRYIGKGTVELONLSSAEVYVPDQTPDENQVYVKIT 540
Oy 541 GHFYACOVAORKIOELITVYKHOQOKALOGSPQSRK 579
Db 541 GHFYACOVAORKIOELITVYKHOQOKALOGSPQSRK 579
```

RESULT 7

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US-09-897-778-446
: Sequence 446, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897.778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ NOS: 467
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 446
: LENGTH: 579
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-897-778-446
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Query Match 99.6% Score 2943: DB 10: Length 579:  
Best Local Similarity 99.7% Pred. No. 9.6e-217:  
Matches 577: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

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Oy 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTKGYAFVDCPDSEMAKAIEMALSG 60
Db 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVTKGYAFVDCPDSEMAKAIEMALSG 60
Oy 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPRLQEWYLDLSLOYGVVSCQVNTDSEFA 120
Db 61 IELHCKPIEVHSHVPRKORIRKLOIRNIPRLQEWYLDLSLOYGVVSCQVNTDSEFA 120
Oy 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Db 121 VNVVYSSKQDARQALDKLNGFOLNFTLKVAYIPDEMAAQNPLQDQGRGRGIGQSGSS 180
Oy 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAIGKAGATIRNITKQOSKIDVHREKENGAA 240
Db 181 ROGSPGVSQKQPCDDPLRLVPTQFVGAIGKAGATIRNITKQOSKIDVHREKENGAA 240
Oy 241 EKSTITLSTPEGTSAACKSILEIMKEADIKFTEELPKLIHNNFVGRIGEGRNK 300
Db 241 EKSTITLSTPEGTSAACKSILEIMKEADIKFTEELPKLIHNNFVGRIGEGRNK 300
Oy 301 KIEODTRKTIISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
Db 301 KIEODTRKTIISPLQELTYNPERTIVKGNVETCAKAEELMKIRESEYENDIASMNL 360
```

Query Match	Similarity	Score	DB	Length
Best Local	99.78%	2943	10	579
Matches	577	Conservative	0	Mismatches
			2	Indels
			0	Gaps
			0	
QY	1	MNKLIGNLSENAPSDLESIFRKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSG	60	
Db	1	MNKLIGNLSENAPSDLESIFRKDAKIPVSGPFLVKTGYAFVDCPDDESMALKAIEALSG	60	
QY	61	IELHGKRIEVEHNSVPRKQRIKRIKQIRNI PPHLOMVLDSLLVQGVGSESCQVNTDSEPA	120	
Db	61	IELHGKRIEVEHNSVPRKQRIKRIKQIRNI PPHLOMVLDSLLVQGVGSESCQVNTDSEPA	120	
QY	121	VVNVNTYSSKQOAAQALDKINGFQLEHFTLKAVY IPDEMAAQNPLQOPRGRGRLGQRGSS	180	
Db	121	VVNVNTYSSKQOAAQALDKINGFQLEHFTLKAVY IPDEMAAQNPLQOPRGRGRLGQRGSS	180	
QY	181	ROGSPGVSQKQPCDPLRLILVPTQFVCAIITGKEGATIRNTTKQTOSKIDVHKRENGAA	240	
Db	181	ROGSPGVSQKQPCDPLRLILVPTQFVCAIITGKEGATIRNTTKQTOSKIDVHKRENGAA	240	
QY	241	EKSTIIILSPREGSAACKSTILEIMHKEODIKFTEEIPILKILANNNVGRLIGKEGKNLK	300	
Db	241	EKSTIIILSPREGSAACKSTILEIMHKEODIKFTEEIPILKILANNNVGRLIGKEGKNLK	300	
QY	301	KIRDDYDKTTTISPOLDELTYLNPERTTVKGNVETCAKAEEIKKIRIESTENDIASMNL	360	
Db	301	KIRDDYDKTTTISPOLDELTYLNPERTTVKGNVETCAKAEEIKKIRIESTENDIASMNL	360	

Query Match	99.4%	Score 2938	DB 10	Length 586
Best Local Similarity	99.7%	Pred. No. 2,3e-216		
Matches 576	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	2	NKLYIGNLSENAAPDLESTIFKQAKIPVSGPPLVYTGAYFYDCEDDSMALKAIEALSKI	61	
Db	9	NKLYIGNLSENAAPDLESTIFKQAKIPVSGPPLVYTGAYFYDCEDDSMALKAIEALSKI	68	
QY	62	ELHGKPIEVEHSVRKORIRKLOIRNIPHLQEWELJSLVQGVGVSCEQVNTQSEFV	121	
Db	69	ELHGKPIEVEHSVRKORIRKLOIRNIPHLQEWELJSLVQGVGVSCEQVNTQSEFV	128	
QY	122	VNNTYSKKQAOALDKINGOLENTLTVAVAPPEMAAOONPLPOOPRGRRIGGQSSR	181	
Db	129	VNNTYSKKQAOALDKINGOLENTLTVAVAPPEMAAOONPLPOOPRGRRIGGQSSR	188	
QY	182	QSGPSGVSKQKFCDLPLRLVPPQFYGALILGEGATINNTIKOTQSKIDYHKKNAGAAE	241	
Db	189	QSGPSGVSKQKFCDLPLRLVPPQFYGALILGEGATINNTIKOTQSKIDYHKKNAGAAE	246	
QY	242	KSTTILSTPEGSTAACKSILEIMHKKEADQIKTEBIPKLIAHNHNVGRLIGKEGRNLK	301	
Db	249	KSTTILSTPEGSTAACKSILEIMHKKEADQIKTEBIPKLIAHNHNVGRLIGKEGRNLK	308	
QY	302	IEEDDTKRTTISPLOEQLTLNPKRTITVYGNVETAKKKEEIMYKIRSEYNDISMLQ	361	
Db	309	IEEDDTKRTTISPLOEQLTLNPKRTITVYGNVETAKKKEEIMYKIRSEYNDISMLQ	366	
QY	362	AHLIRPLNINLALGFPFPGSGMPPTGPGPSAMTPPYPOFQDSSELYVNOFTALSVGAI	421	
Db	369	AHLIRPLNINLALGFPFPGSGMPPTGPGPSAMTPPYPOFQDSSELYVNOFTALSVGAI	428	
QY	422	GKQGHNIKQLSRFKAGASIKTAPAEADAVVRNVIITGPEPQKRAOGRTYGIKKEENFS	481	
Db	429	GKQGHNIKQLSRFKAGASIKTAPAEADAVVRNVIITGPEPQKRAOGRTYGIKKEENFS	488	

Thu Apr 17 07:55:18 2003

us-09-897-778-176.rapb

Page 6

[illegible]

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RESULT 10.
US-09-897-778-427
Sequence 427, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Manerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Matenabe, Yoshitomo
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 427
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-427

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Query Match	Similarity	Score	Pos.38	DB	10	Length	586:
Best Local	Similarity	99.78:	Pred.	No.2	3.e-216:		
Matches	576:	Conservative	0:	Mismatches	2:	Indels	0: Gaps
Oy	2	NKLYTGNLSNMA	PSDLEISIRKDKAI	IPVSGPFLVKTSTGYAVFC	QDPESMAKLAIEALSGKI	61	
Db	9	NKLYTGNLSNMA	PSDLEISIRKDKAI	IPVSGPFLVKTSTGYAVFC	QDPESMAKLAIEALSGKI	68	
Oy	62	ELHGPLEIVHSVPRKQRI	RIRKQIRKIQIRN	PIPHIQMEVLSL	LYQGVVESCEDQVMTDESTAV	121	
Db	69	ELHGPLEIVHSVPRKQRI	RIRKQIRN	PIPHIQMEVLSL	LYQGVVESCEDQVMTDESTAV	128	
Oy	122	VWVYSSKDOARQALDK	INGSOLENTFLVAV	ITFDEMAAOQNP	IQDQPGRRGIGQGGSSR	181	
Db	129	VWVYSSKDOARQALDK	INGSOLENTFLVAV	ITFDEMAAOQNP	IQDQPGRRGIGQGGSSR	188	
Oy	182	QSPSPVSKKRCQDPL	PLVLPYQFGALIT	IGEGEATIRNT	KOTOSKIDYHRENNAGAE	241	
Db	189	QSPSPVSKKRCQDPL	PLVLPYQFGALIT	IGEGEATIRNT	KOTOSKIDYHRENNAGAE	248	
Oy	242	KSTITLSPGTSACKS	SLIEIMKRAQDIKTET	PIKLIAHNPVRL	GLGEGENLKK	301	
Db	249	KSTITLSPGTSACKS	SLIEIMKRAQDIKTET	PIKLIAHNPVRL	GLGEGENLKK	308	
Oy	302	IQDDIDPKITISL	LOELTLNPEKTTIV	GANVENCANAAEEL	IMKIRISRYENDIASMNLQ	361	
Db	309	IQDDIDPKITISL	LOELTLNPEKTTIV	GANVENCANAAEEL	IMKIRISRYENDIASMNLQ	368	
Oy	362	AHLITPGNLNALG	LEPPTSGMPPTSGP	SPSANTPPYQF	FOSETETVHQITPALSYGATI	421	
Db	369	AHLITPGNLNALG	LEPPTSGMPPTSGP	SPSANTPPYQF	FOSETETVHQITPALSYGATI	428	
Oy	422	GKQGHKIKOLSRPAGASIK	INAPADAPAVRVV	VIITSPBPAQKAGNI	YGIKEENFVS	481	
Db	429	GKQGHKIKOLSRPAGASIK	INAPADAPAVRVV	VIITSPBPAQKAGNI	YGIKEENFVS	488	

[illegible]

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RESULT 11
US-09-873-637-2
Sequence 2, Application US/09873637
Patent No. US20020061543A1
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296, 95131
CURRENT APPLICATION NUMBER: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ. ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO. 2
LENGTH: 577
TYPE: prt
ORGANISM: Mus musculus
US-09-873-637-2

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[illegible]

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RESULT 12
US-09-764-864-1116
; Sequence 1116, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1116
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (533)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1116

Query Match          65.8%; Score 1946.5; DB 10; Length 620;
Best Local Similarity 65.1%; Pred. No. 1.5e-140;
Matches 385; Conservative 81; Mismatches 96; Indels 29; Gaps 8;

OY 1 MNKLYIGNLSENPASDLESIFKDAKIPVSGPLVGYAFVDCPDSEWALKAIEALSG 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 23 MNKLYIGNLSPAVYADLRFQDRKPLLAGVLLKSGAFADYDPQNNATIAITLSGK 82
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 61 TELGKPLEVSHVPRQRIRKIQIRINIPHLOWEVLDSLVGYGVESCEOVNTDSTA 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 83 VELHKIMEVDYSVKLRKIRKIQIRINIPHLOWEVLDSLVGYGVENVDGNTDETA 142
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 121 VVNTYSSKDAQARALDKINGFPLENTFLKAVIIPDEMAQONPQQPRGRGLGQRRSS 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 143 VVNTYATREAKTAMKLSGHOPEYSEKISTIPDEYSSPSPP--RAQR--GDHSR 198
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 181 ROG-SPGSVSKOKPDLPLRLVPTQFVCAITGREGATIRNTKOTOSKIDVHRKENAGA 239
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 199 EOGNAPGSGTSQARQIDPPLRLVPTQFVCAITGREGATIRNTKOTOSKIDVHRKENAGA 258
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 240 AEKSTILSPRGTSACKSILEIMHKEODIKFTEIRPLKILAHNPFGRILGEGENL 299
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 259 AEKPTTHATPEGTSEACRMILEIMHKEADETKLAEIPLKILAHNPFGRILGEGENL 318
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 300 KKEODPTDKITISPLQELTLYNPERTITVKNVETCANAEEMIKKIRESENDIASMN 359
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 319 KKEHEGTKITISSLODLSIYNERITVKGIVEACASAEIEMKRLREAFENMLAVN 378
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 360 LOAHILPOLNINALGLF-----PPTS--GMPPT-----SGPPSAMTP-----P 396
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 379 QOANILIPOLNINLALGLFSTGLSVLSPAGPRGAPAPAPHPFTTHGYSSTLYPHHOGFP 438
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 397 YPOFQO--SETETVHOFTPALSVGAILIGKOGHITKOLSRFAGASIKIAPAEADAVRWYI 455
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 439 FPHHSTYFQETIVMLFTPTQAVGAILIGKOGHITKOLSRFAGASIKIAPAEADAVRWYI 498
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 456 ITGPEPAQFAQGRIRYKIRKEENFVSPKEEVKLEAHIRVPSFAAGVIGKGTAVNELON 515
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 499 ITGPEPAQFAQGRIRYKIRKEENFVSPKEEVKLEAHIRVPSFAAGVIGKGTAVNELON 558
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 516 LSSAVVVPVPRQTPDENDDVVYKITGHFYACQVAKRKIQELIOLTVQKHOOO 566
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 559 LTSAEVVPVPRQTPDENDDVVYKITGHFYACQVAKRKIREIYQVQVQDQDOK 609
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
US-09-764-864-1114
; Sequence 1114, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1114
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1114

Query Match          32.1%; Score 949; DB 10; Length 261;
Best Local Similarity 74.5%; Pred. No. 6.9e-65;
Matches 193; Conservative 26; Mismatches 32; Indels 8; Gaps 5;

OY 324 ERTIVKGNVETCAKAEIEIKKIRESENDIASMNLOAHILPOLNINLALGLFPPTSGMP 383
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 8 ERTIVKGAIENCRAEIOEIMKKVKEAVENDVAAASLOSHLIPGLNLAAGLEFPASSAV 67
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 384 PPTSGPPSAMT--PPYPOFQO--ETETVHOFTPALSVGAILIGKOGHITKOLSRFAGASIK 440
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 68 PP---PPSVTGAATYSSFPQAPPEDEMVOYTPQAVGAILIGKOGHITKOLSRFAGASIK 124
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 441 IAPAEAPDAKVMVITITGPEPAQFAQGRIRYKIRKEENFVSPKEEVKLEAHIRVPSFAAG 500
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 125 IAPETPDSKVMVITITGPEPAQFAQGRIRYKIRKEENFVSPKEEVKLEAHIRVPSFAAG 184
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 501 RYIGKGGKTVNLOLSSAEVVPVPRQTPDENDDVVYKITGHFYACQVAKRKIQELIOLTV 560
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 185 RYIGKGGKTVNLOLSSAEVVPVPRQTPDENDDVVYKITGHFYACQVAKRKIRDLAAY 244
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY 561 KOHQOQKALQSGPPQSRKK 579
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 245 KO-QHQKG-QSNQAQARRK 261
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
US-09-764-864-1532
; Sequence 1532, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1532
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (134)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1532

Query Match          31.1%; Score 919; DB 10; Length 250;
Best Local Similarity 73.3%; Pred. No. 1.3e-62;
Matches 187; Conservative 26; Mismatches 34; Indels 8; Gaps 5;

OY 328 TVKGNVETCAKAEIEIKKIRESENDIASMNLOAHILPOLNINLALGLFPPTSGMPPTS 387
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 TVKGAIENCRAEIOEIMKKVKEAVENDVAAASLOSHLIPGLNLAAGLEFPASSAVPP-- 58
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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OY 388 GPPSAMT--PYPPOFOS-ETETVHOFIPALSGAIIIGKOGHIOKLSRFAGASIKIAPA 444
DB 59 -PPSSVTGAAPFSSFMQAPDEQEMQVFIIPAQVGAIIIGKOGHIOKLSRFASASIKIAPP 117
OY 445 EAPDAKVRVYIITGPPEOQFAOGRIYKIKENFVSPKKEVKLEAHIRVPSFAAGRVIG 504
DB 118 ETPDSKVRXIIITCPXAQKQACQRIYKIKLEENFGPKKEVKLETHIRVPASACRVIG 177
OY 505 KGGKTVNELQNLSSAEVVVPRDQTPDENDDVYVKTGHFACOVAAQRKIOTETITOVKOHQ 564
DB 178 KGGKTVNELQNLSSAEVVVPRDQTPDENDDVYVKTGHFACOVAAQRKIOTETITOVKOHQ 236
OY 565 QOKALQSGPPOSRRK 579
DB 237 HOKG-OSNOQAARK 250
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RESULT 15
US-09-764-864-1119
; Sequence 1119, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001.01.17
; PUBLICATION DATE: 2002.01.17
; NUMBER OF SEQ. ID NOS.: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO. 1119
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1119
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Query Match 21.2%; Score 626; DB 10; Length 171;  
Best Local Similarity 80.5%; Pred. No. 1.8e-40;  
Matches 120; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

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OY 418 GAIGKOGHIOKLSRFAGASIKIAPAEPADKVRVYIITGPPEOQFAOGRIYKIKEE 477
DB 12 GAIGKOGHIOKLSRFAGASIKIAPAEQPVSEKRVYIITGPPEOQFAOGRIYKIKEE 71
OY 478 NFVSPKKEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDDVYV 537
DB 72 NFVSPKKEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDDVYV 131
OY 538 KITGHFACOVAAQRKIOTETITOVKOHQ 566
DB 132 KITGHFACOVAAQRKIOTETITOVKOHQ 160
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Search completed: April 16, 2003, 16:32:11  
Job time : 45.734 secs



1	2956	100.0	579	6	US-10-313-986-176	Sequence 176, Ap
2	2956	100.0	579	6	US-10-348-119-255	Sequence 248, Ap
3	2943	99.6	579	6	US-10-313-986-345	Sequence 348, Ap
4	2943	99.6	579	6	US-10-313-986-446	Sequence 446, Ap
5	2943	99.6	579	6	US-10-313-986-449	Sequence 449, Ap
6	2943	99.6	579	6	US-10-313-986-440	Sequence 480, Ap
7	2943	99.6	589	6	US-10-313-986-486	Sequence 486, Ap
8	2938	99.4	586	6	US-10-313-986-427	Sequence 427, Ap
9	2937	99.4	579	6	US-10-313-986-484	Sequence 484, Ap
10	2826	95.6	558	5	US-09-724-676-92918	Sequence 92918, Ap
11	2826	95.6	558	5	US-09-724-676-92918	Sequence 92918, Ap
12	2459.5	83.2	492	5	US-09-724-676-92916	Sequence 92916, Ap
13	2459.5	83.2	492	5	US-09-724-676-92916	Sequence 92916, Ap
14	2191	74.1	577	6	US-10-313-986-500	Sequence 500, Ap
15	2112	71.4	572	5	US-09-724-676-48617	Sequence 48617, Ap
16	2112	71.4	572	5	US-09-724-676-48618	Sequence 48618, Ap
17	2112	71.4	572	5	US-09-724-676-48617	Sequence 48617, Ap
18	2112	71.4	572	5	US-09-724-676-48618	Sequence 48618, Ap
19	2105.5	71.2	602	5	US-09-724-676-48619	Sequence 48619, Ap
20	2105.5	71.2	602	5	US-09-724-676-48620	Sequence 48620, Ap
21	2105.5	71.2	602	5	US-09-724-676-48620	Sequence 48619, Ap
22	2105.5	71.2	602	5	US-09-724-676-48620	Sequence 48620, Ap
23	2069	70.7	598	5	US-09-724-676-48616	Sequence 48616, Ap
24	2089	70.7	598	5	US-09-724-676-48621	Sequence 48621, Ap
25	2089	70.7	598	5	US-09-724-676-48616	Sequence 48616, Ap
26	2089	70.7	598	5	US-09-724-676-48621	Sequence 48621, Ap

Db 301 KIEQDTKITSPLQ

Db 301 KIEQDTKITISPLQELTYNPERTIVKGNVETCAKAEIEIMKKIRESYENDIASMNL, 360

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Page 2

Qy	361	QALHGLNLANLGIPTSGMPPTSGPSPMPPTSGPQSGSTETVHOFIPALISVAI	420
Dp	361	QALLPGLNLANLGIPTSGMPPTSGPSPMPPTSGPQSGSTETVHOFIPALISVAI	420
Qy	421	IGGQGHGKOLSPRPAASIKILAPAPADKAYMYITIGPEAPQFKQAGIYKIKENFV	480
Dp	421	IGKQSHGILQSRFPAASIKILAPAPADKAYMYITIGPEAPQFKQAGIYKIKENFV	480
Qy	481	SPPEEYKLEAHIRVPSFPAAGRVIGKGGKTVNELNLSSAEVYVPRDPTDENDQVYKIT	540
Dp	481	SPPEEYKLEAHIRVPSFPAAGRVIGKGGKTVNELNLSSAEVYVPRDPTDENDQVYKIT	540
Qy	541	GHEFYACVAQRKIQEILTVQKHQOQKALQSPQSRK	579
Dp	541	GHEFYACVAQRKIQEILTVQKHQOQKALQSPQSRK	579

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RESULT 2
US-10-348-119-255
: Sequence 255, Application US/10348119
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
: TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES
: TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
: FILE REFERENCE: D0185 NP
: CURRENT APPLICATION NUMBER: US/10/348.119
: CURRENT FILING DATE: 2003-01-17
: PRIOR APPLICATION NUMBER: US 60/350,061
: PRIOR FILING DATE: 2002-01-18
: NUMBER OF SEQ ID NOS: 795
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO: 255
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-348-119-255

```

Query Match	100.0%	Score 2956	DB 6	Length 579
Best Local Similarity	100.0%	Pred. No. 4e-244		
Matches 579	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MNLTGYNLSENAAPSDLESIFRKDAKIPVSGFELTKGVAFVCCPESNALAKAIATASGK	60	
Db	1	MNLTGYNLSENAAPSDLESIFRKDAKIPVSGFELTKGVAFVCCPESNALAKAIATASGK	60	
QY	61	IELHGKPIFIVESEVPKRORIKIQIRNIPPHOMVEVDLSLVOYGAVESCEQVNMDSSTA	120	
Db	61	IELHGKPIFIVESEVPKRORIKIQIRNIPPHOMVEVDLSLVOYGAVESCEQVNMDSSTA	120	
QY	121	VVVVTVSSKDOARALNKLNGFOLNFTLKVAYIDEKAAQNPLOQPPGRGLGLORSS	180	
Db	121	VVVVTVSSKDOARALNKLNGFOLNFTLKVAYIDEKAAQNPLOQPPGRGLGLORSS	180	
QY	181	ROSPSPSVSKORPDDLRLRLVPTQFVGAIICKBEATIRNITQOTSKIDVHRKKNAAGA	240	
Db	181	ROSPSPSVSKORPDDLRLRLVPTQFVGAIICKBEATIRNITQOTSKIDVHRKKNAAGA	240	
QY	241	EKSITLLSPGEGTSNAACKSLLEIMHKEADIKFTEIEIPKLILAHNMFVRLIGCKGRMLK	300	
Db	241	EKSITLLSPGEGTSNAACKSLLEIMHKEADIKFTEIEIPKLILAHNMFVRLIGCKGRMLK	300	
QY	301	KIEODIDRKITISPLQELTLYNPERTIYKGVETCAKAAEBEIMKKIRSESYNDIDVSNML	360	
Db	301	KIEODIDRKITISPLQELTLYNPERTIYKGVETCAKAAEBEIMKKIRSESYNDIDVSNML	360	
QY	361	QAHLLPGNLNALALFPPTSGMPPTSGSPASAMPVPVPOFEOSETVTVQOIFPALSVYAI	420	
Db	361	QAHLLPGNLNALALFPPTSGMPPTSGSPASAMPVPVPOFEOSETVTVQOIFPALSVYAI	420	
QY	421	ICKGCOHAKOLSRFAGASIKIAPAEAPDAKVMVITVGPDAQFKAGZIRYIKIKEENFV	480	
Db	421	ICKGCOHAKOLSRFAGASIKIAPAEAPDAKVMVITVGPDAQFKAGZIRYIKIKEENFV	480	

Db	421	IGGGGHIKQLSTRPASA	SIKIAPIAEADAVKRVIIITSPPEAKGKAGRIYKIEENFV	5408
QY	481	SRKEEVKILEAIRPSPFA	GRYKRGKTVNELKQLISSAEVYVPRDPTDPENDQYVNT	5408
Db	481	SRKEEVKILEAIRPSPFA	GRYKRGKTVNELKQLISSAEVYVPRDPTDPENDQYVNT	5408
QY	541	GHFYACQAGKRIQELIT	LYVKKHQKQALQSPGSRK	579
Db	541	GHFYACQAGKRIQELIT	LYVKKHQKQALQSPGSRK	579

```

RESULT 3
US-10-313-986-348
; Sequence 348, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andrea
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ. ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ. ID NO. 348
LENGTH: 579
TYPE: PRY
ORGANISM: Homo sapiens
US-10-313-986-348

```

Query Match	Similarity	99.6%	Score 2943	DB.6:	Length 579:
Best Local	Similarity	99.7%	Pred. No. 5.2e-243:		
Matches 577:	Conservative	0:	Mismatches	2:	Indels 0: Gaps 0:
Qy	1	MNLYGNISEMAAPSDLESIFPKDAKIPVSGGPIYKTVGAFAVCCPSPSALKAIETALSG	60		
Dh	1	MNLYGNISEMAAPSDLESIFPKDAKIPVSGGPIYKTVGAFAVCCPSPSALKAIETALSG	60		
Qy	61	IELHGKPIEVEHSVPKRRQIRKQIINIPHLOWEVDLSLLVGYGVESCEQVNDSETA	120		
Dh	61	IELHGKPIEVEHSVPKRRQIRKQIINIPHLOWEVDLSLLVGYGVESCEQVNDSETA	120		
Qy	121	VVVVVYSKDKARALDLKNGFLENFTYKAVYIPDEMAAQNPLDQPGRGGLQGRSS	180		
Dh	121	VVVVVYSKDKARALDLKNGFLENFTYKAVYIPDEMAAQNPLDQPGRGGLQGRSS	180		
Qy	181	ROGSPGVSVKORPCDPLRLVLPFGVAGIIGKEGATIRNTKOTSKIDYHRKENGAA	240		
Dh	181	ROGSPGVSVKORPCDPLRLVLPFGVAGIIGKEGATIRNTKOTSKIDYHRKENGAA	240		
Qy	241	EKSITITLSPGTSACKSTLEILMKKEADIKFIBELPIKLIAHNNFVGRILGKEGRNLK	300		
Dh	241	EKSITITLSPGTSACKSTLEILMKKEADIKFIBELPIKLIAHNNFVGRILGKEGRNLK	300		
Qy	301	KIROPDPKRTISPLQELTYNPEERTYKGVGKATCAAEETIMKPIPSYNDLASMNL	360		
Dh	301	KIROPDPKRTISPLQELTYNPEERTYKGVGKATCAAEETIMKPIPSYNDLASMNL	360		
Qy	361	QAILPLDGLNALALPPTSGMPPTSGSPSAMPVPRQEGSESTYHOPFALISGAI	420		
Dh	361	QAILPLDGLNALALPPTSGMPPTSGSPSAMPVPRQEGSESTYHOPFALISGAI	420		
Qy	421	IGKOGGHIKOLSRFAGASTIAPAEAPDAKRVMTYINGPEAPFKOGGRTGKIKENPV	480		
Dh	421	IGKOGGHIKOLSRFAGASTIAPAEAPDAKRVMTYINGPEAPFKOGGRTGKIKENPV	480		
Qy	481	SPPEEUKLEAHIRVPSFAAGRVYIGKGGKRYVELNLSSAEVVVPVPROTFDEKDQVYVIT	540		
Dh	481	SPPEEUKLEAHIRVPSFAAGRVYIGKGGKRYVELNLSSAEVVVPVPROTFDEKDQVYVIT	540		

Oy 541 GHFYACVAAORAKIOEILITGVKHOQOAKALQSGPPOSRRK 579  
Db 541 GHFYACVAAORAKIOEILITGVKHOQOAKALQSGPPOSRRK 579

RESULT 4  
US-10-313-986-446  
; Sequence 446, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C19  
; CURRENT APPLICATION NUMBER: US/10/313,986  
; CURRENT FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 446  
; LENGTH: 579  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-313-986-446

Query Match 99.6%; Score 2943; DB 6; Length 579;  
Best Local Similarity 99.7%; Pred. No. 5.2e-243;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MNKLYIGNLSENNAPSDLESIFDKAKIPVSGPFLVKTGYAFVDDPDESMALKATEALSGK 60  
Db 1 MNKLYIGNLSENNAPSDLESIFDKAKIPVSGPFLVKTGYAFVDDPDESMALKATEALSGK 60  
Oy 61 IELHGRPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSETA 120  
Db 61 IELHGRPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSETA 120  
Oy 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Db 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Oy 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Db 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Oy 181 RQSGPSSVSKQPCDPLRLVLPVTFVGAIIKGEKATIRNITKQTSKIDVHREKNGAA 240  
Db 181 RQSGPSSVSKQPCDPLRLVLPVTFVGAIIKGEKATIRNITKQTSKIDVHREKNGAA 240  
Oy 241 EKSTIIITSTPEGTSACKSILEIMHKEADIKFTEIPIKLILAHNPFVGRILIGEGRNK 300  
Db 241 EKSTIIITSTPEGTSACKSILEIMHKEADIKFTEIPIKLILAHNPFVGRILIGEGRNK 300  
Oy 301 KIEDDTFKITISPLQELFLYNPERTITVKGWETCAKAEEMKIRESEYENDIASMNL 360  
Db 301 KIEDDTFKITISPLQELFLYNPERTITVKGWETCAKAEEMKIRESEYENDIASMNL 360  
Oy 361 QAHILIPGINNALGLPPTSGMPPTSGPSAMTPPYQFQFQSETEYHOFIPALSGAI 420  
Db 361 QAHILIPGINNALGLPPTSGMPPTSGPSAMTPPYQFQFQSETEYHOFIPALSGAI 420  
Oy 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Db 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Oy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVYVPPDDQTPDENDDVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVYVPPDDQTPDENDDVYVKIT 540  
Oy 541 GHFYACVAAORAKIOEILITGVKHOQOAKALQSGPPOSRRK 579  
Db 541 GHFYACVAAORAKIOEILITGVKHOQOAKALQSGPPOSRRK 579

RESULT 5

US-10-313-986-449  
; Sequence 449, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tonglong  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C19  
; CURRENT APPLICATION NUMBER: US/10/313,986  
; CURRENT FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 449  
; LENGTH: 579  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-313-986-449

Query Match 99.6%; Score 2943; DB 6; Length 579;  
Best Local Similarity 99.7%; Pred. No. 5.2e-243;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MNKLYIGNLSENNAPSDLESIFDKAKIPVSGPFLVKTGYAFVDDPDESMALKATEALSGK 60  
Db 1 MNKLYIGNLSENNAPSDLESIFDKAKIPVSGPFLVKTGYAFVDDPDESMALKATEALSGK 60  
Oy 61 IELHGRPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSETA 120  
Db 61 IELHGRPIEVEHSPVKRQRIKQIRNIPPHLOMEVLDLSLVGYGVSECEQVNTDSETA 120  
Oy 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Db 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Oy 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Db 121 VVNTYSSKQOARQALDKLNGFQLENFTLKAVYIPDEMAAQNPLQOPRGRRGLGOGSS 180  
Oy 181 RQSGPSSVSKQPCDPLRLVLPVTFVGAIIKGEKATIRNITKQTSKIDVHREKNGAA 240  
Db 181 RQSGPSSVSKQPCDPLRLVLPVTFVGAIIKGEKATIRNITKQTSKIDVHREKNGAA 240  
Oy 241 EKSTIIITSTPEGTSACKSILEIMHKEADIKFTEIPIKLILAHNPFVGRILIGEGRNK 300  
Db 241 EKSTIIITSTPEGTSACKSILEIMHKEADIKFTEIPIKLILAHNPFVGRILIGEGRNK 300  
Oy 301 KIEDDTFKITISPLQELFLYNPERTITVKGWETCAKAEEMKIRESEYENDIASMNL 360  
Db 301 KIEDDTFKITISPLQELFLYNPERTITVKGWETCAKAEEMKIRESEYENDIASMNL 360  
Oy 361 QAHILIPGINNALGLPPTSGMPPTSGPSAMTPPYQFQFQSETEYHOFIPALSGAI 420  
Db 361 QAHILIPGINNALGLPPTSGMPPTSGPSAMTPPYQFQFQSETEYHOFIPALSGAI 420  
Oy 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Db 421 IKGOGHILKOLSRFAGASIKIAPAEAPDAKVMVITITGPEAOFKAGRIYGIKEENFV 480  
Oy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVYVPPDDQTPDENDDVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELONLSAEVYVPPDDQTPDENDDVYVKIT 540  
Oy 541 GHFYACVAAORAKIOEILITGVKHOQOAKALQSGPPOSRRK 579  
Db 541 GHFYACVAAORAKIOEILITGVKHOQOAKALQSGPPOSRRK 579

RESULT 6  
US-10-313-986-480  
; Sequence 480, Application US/10313986  
; GENERAL INFORMATION:  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: McNabb, Andria  
; APPLICANT: Matanabe, Yoshihiro

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; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-480

Query Match          99.6%; Score 2943; DB 6; Length 579;
Best Local Similarity 99.7%; Pred. No. 5.2e-243;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKATLSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKATLSGK 60
QY 61 IELHCKPIEVESHVPKRRORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
DB 61 IELHCKPIEVESHVPKRRORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
QY 121 VVNVYSSKDOAROLDKLNQFQLENFTLKVAAYIPDEMAAQQNPLOOPGRRGGLGGRSS 180
DB 121 VVNVYSSKDOAROLDKLNQFQLENFTLKVAAYIPDEMAAQQNPLOOPGRRGGLGGRSS 180
QY 181 RQSGPSVSKQPCDDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENGAA 240
DB 181 RQSGPSVSKQPCDDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENGAA 240
QY 241 EKSITILSTPEGTSAACKSILEIMHKEADIKFTEETPLKILAHNNFVRLIGKEGRMLK 300
DB 241 EKSITILSTPEGTSAACKSILEIMHKEADIKFTEETPLKILAHNNFVRLIGKEGRMLK 300
QY 301 KIEQDTDKITISPLQELTLYNPERTIVKGNVETCAKAEETIMKKIRSEYENDIASNML 360
DB 301 KIEQDTDKITISPLQELTLYNPERTIVKGNVETCAKAEETIMKKIRSEYENDIASNML 360
QY 361 QAHILPGLNLTALGLFPTSGMPPTSGPPSAMTPPYPOEJOSETETVHLFPALSVGAI 420
DB 361 QAHILPGLNLTALGLFPTSGMPPTSGPPSAMTPPYPOEJOSETETVHLFPALSVGAI 420
QY 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFKQOGITYKIKEENFV 480
DB 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFKQOGITYKIKEENFV 480
QY 481 SKREEVKLEAHIRVPSAAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
DB 481 SKREEVKLEAHIRVPSAAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
QY 541 GHFYACGYAORKIOELITTOVKOHQOQKALQSGPPQSRK 579
DB 541 GHFYACGYAORKIOELITTOVKOHQOQKALQSGPPQSRK 579

RESULT 7
US-10-313-986-486
; Sequence 486, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
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; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 486
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-486

Query Match          99.6%; Score 2943; DB 6; Length 589;
Best Local Similarity 99.7%; Pred. No. 5.3e-243;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKATLSGK 60
DB 1 MNKLYIGNLSENAPSDLESIFKDAKIPVSGPFLVKTGVAFVDCPDSEWALKATKATLSGK 60
QY 61 IELHCKPIEVESHVPKRRORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
DB 61 IELHCKPIEVESHVPKRRORIRKIQIRNIPPHLOMEVLDLSLVGYGVESCEQVNTDSETA 120
QY 121 VVNVYSSKDOAROLDKLNQFQLENFTLKVAAYIPDEMAAQQNPLOOPGRRGGLGGRSS 180
DB 121 VVNVYSSKDOAROLDKLNQFQLENFTLKVAAYIPDEMAAQQNPLOOPGRRGGLGGRSS 180
QY 181 RQSGPSVSKQPCDDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENGAA 240
DB 181 RQSGPSVSKQPCDDPLRLVPTQFVGAIIIGKEGATIRNITKOTOSKIDVHRKENGAA 240
QY 241 EKSITILSTPEGTSAACKSILEIMHKEADIKFTEETPLKILAHNNFVRLIGKEGRMLK 300
DB 241 EKSITILSTPEGTSAACKSILEIMHKEADIKFTEETPLKILAHNNFVRLIGKEGRMLK 300
QY 301 KIEQDTDKITISPLQELTLYNPERTIVKGNVETCAKAEETIMKKIRSEYENDIASNML 360
DB 301 KIEQDTDKITISPLQELTLYNPERTIVKGNVETCAKAEETIMKKIRSEYENDIASNML 360
QY 361 QAHILPGLNLTALGLFPTSGMPPTSGPPSAMTPPYPOEJOSETETVHLFPALSVGAI 420
DB 361 QAHILPGLNLTALGLFPTSGMPPTSGPPSAMTPPYPOEJOSETETVHLFPALSVGAI 420
QY 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFKQOGITYKIKEENFV 480
DB 421 IKGOGOHIKOLSRFAGASIKIAPAEAPDAKVRMVIITGPEAOFKQOGITYKIKEENFV 480
QY 481 SKREEVKLEAHIRVPSAAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
DB 481 SKREEVKLEAHIRVPSAAGRVYIGKGTVNEQLNLSAEVVVPRQOTDEDDQVYVKT 540
QY 541 GHFYACGYAORKIOELITTOVKOHQOQKALQSGPPQSRK 579
DB 541 GHFYACGYAORKIOELITTOVKOHQOQKALQSGPPQSRK 579

RESULT 8
US-10-313-986-427
; Sequence 427, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-313-986-427

Query Match          99.4%; Score 2938; DB 6; Length 586;
Best Local Similarity 99.7%; Pred. No. 1.4e-242;
Matches 576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKLTYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSCK 61
    |||
DB 9 NKLTYGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSCK 68
QY 62 ELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYDLSLVQYGVESCEQVNTDSETA 121
    |||
DB 69 ELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYDLSLVQYGVESCEQVNTDSETA 128
QY 122 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQQNPLOQPRGRGLGGRGSS 181
    |||
DB 129 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQQNPLOQPRGRGLGGRGSS 188
QY 182 QSPGSGSVKQKCDLPLRLVPTQFVGAITGEGATIRNITQOTOSKIDVHRKENAGAA 241
    |||
DB 189 QSPGSGSVKQKCDLPLRLVPTQFVGAITGEGATIRNITQOTOSKIDVHRKENAGAA 248
QY 242 KSITTLSTPEGTSAAKSIILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGEGRNLLK 301
    |||
DB 249 KSITTLSTPEGTSAAKSIILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGEGRNLLK 308
QY 302 IEODDTTKITISPLQELTLYNPERRITVKGAVETCAKAEELIMKKIRSEYENDIASMNLQ 361
    |||
DB 309 IEODDTTKITISPLQELTLYNPERRITVKGAVETCAKAEELIMKKIRSEYENDIASMNLQ 368
QY 362 AHLIPGLNINLALGFPPTSGMPPTSGPPSANTPPYPOEJOSETETVHOFTIPALSVGAI 421
    |||
DB 369 AHLIPGLNINLALGFPPTSGMPPTSGPPSANTPPYPOEJOSETETVHOFTIPALSVGAI 428
QY 422 GKOGQHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPEPAQFKAGRIYKIKEENFV 481
    |||
DB 429 GKOGQHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPEPAQFKAGRIYKIKEENFV 488
QY 482 PKEEVKLEAHIRVPSFAAGRVIGKGGKTYNELONLSAENVVPROTDENDOVVVKITG 541
    |||
DB 489 PKEEVKLEAHIRVPSFAAGRVIGKGGKTYNELONLSAENVVPROTDENDOVVVKITG 548
QY 542 HFYACOVAORKTIOELITOVKHOQKALOSGPPQSRK 579
    |||
DB 549 HFYACOVAORKTIOELITOVKHOQKALOSGPPQSRK 586

RESULT 9
US-10-313-986-484
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 579
; TYPE: PRT
; ORGANISM: primate
US-10-313-986-484

Query Match          99.4%; Score 2937; DB 6; Length 579;
Best Local Similarity 99.3%; Pred. No. 1.7e-242;
Matches 575; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSCK 60
    |||
DB 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSCK 60
QY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYDLSLVQYGVESCEQVNTDSETA 120
    |||
DB 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYDLSLVQYGVESCEQVNTDSETA 120
QY 121 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQQNPLOQPRGRGLGGRGSS 180
    |||
DB 121 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQQNPLOQPRGRGLGGRGSS 180
QY 181 ROSPGSGSVKQKCDLPLRLVPTQFVGAITGEGATIRNITQOTOSKIDVHRKENAGAA 240
    |||
DB 181 ROSPGSGSVKQKCDLPLRLVPTQFVGAITGEGATIRNITQOTOSKIDVHRKENAGAA 240
QY 241 EKSTTLSTPEGTSAAKSIILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGEGRNLLK 300
    |||
DB 241 EKSTTLSTPEGTSAAKSIILEIMHKEADIKFTEEIPKLILAHNNFVGRLLGEGRNLLK 300
QY 301 KIEODDTTKITISPLQELTLYNPERRITVKGAVETCAKAEELIMKKIRSEYENDIASMNL 360
    |||
DB 301 KIEODDTTKITISPLQELTLYNPERRITVKGAVETCAKAEELIMKKIRSEYENDIASMNL 360
QY 361 AHLIPGLNINLALGFPPTSGMPPTSGPPSANTPPYPOEJOSETETVHOFTIPALSVGAI 420
    |||
DB 361 AHLIPGLNINLALGFPPTSGMPPTSGPPSANTPPYPOEJOSETETVHOFTIPALSVGAI 420
QY 421 IGKOGQHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPEPAQFKAGRIYKIKEENFV 480
    |||
DB 421 IGKOGQHIKOLSRFAGASIKIAPAEAPDAKVRWVITGPEPAQFKAGRIYKIKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTYNELONLSAENVVPROTDENDOVVVKIT 540
    |||
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTYNELONLSAENVVPROTDENDOVVVKIT 540
QY 541 GHFYACOVAORKTIOELITOVKHOQKALOSGPPQSRK 579
    |||
DB 541 GHFYACOVAORKTIOELITOVKHOQKALOSGPPQSRK 579

RESULT 10
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match          95.6%; Score 2826; DB 5; Length 558;
Best Local Similarity 99.8%; Pred. No. 5e-233;
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSCK 60
    |||
DB 1 MNKLYIGNLSNAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIEALSCK 60
QY 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYDLSLVQYGVESCEQVNTDSETA 120
    |||
DB 61 IELHGKPIEVESHVPRKQRIKRLQIRNIPPHLOWEYDLSLVQYGVESCEQVNTDSETA 120
QY 121 VNVVYSSKQAOALDKLNGFOLNFTLKVAIIPDEMAAQQNPLOQPRGRGLGGRGSS 180
    |||

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Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGQRSS 180  
QY 181 RQSPGVSYSKQPCDPLRLVLPTQFVGAIIKGGATIRNTKOTQSKIDVHKENAGAA 240  
Db 181 RQSPGVSYSKQPCDPLRLVLPTQFVGAIIKGGATIRNTKOTQSKIDVHKENAGAA 240  
QY 241 EKSTIILSTPEGTSAAKCSILEIMHKEADIKFTEEIPKILAHNNFVGRILGKEGRNLK 300  
Db 241 EKSTIILSTPEGTSAAKCSILEIMHKEADIKFTEEIPKILAHNNFVGRILGKEGRNLK 300  
QY 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360  
Db 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360  
QY 361 QAHILPGNLNMGLEFPPTSGMPPTSGPSAMTPPYPOFQSETEYVHOFTIPALSVGAI 420  
Db 361 QAHILPGNLNMGLEFPPTSGMPPTSGPSAMTPPYPOFQSETEYVHOFTIPALSVGAI 420  
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMTITGPPEAQFKAGRTIGKIEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMTITGPPEAQFKAGRTIGKIEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAGAVIGKGTYNELQNTSSAEVYVPDQTPDENDQVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGAVIGKGTYNELQNTSSAEVYVPDQTPDENDQVYVKIT 540  
QY 541 GHFYACQVAORIKQ 554  
Db 541 GHFYACQVAORIKR 554

## RESULT 11

US-09-724-676A-92918  
Sequence 92918 Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92918

Query Match 95.68; Score 2826; DB 5; Length 558;  
Best Local Similarity 99.88; Pred. No. 5e-233;  
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDESIFDKAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAAPSDESIFDKAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60  
QY 61 IELHCKPIEVEHSVKKRQRIKRLQIRNIPHLQMEVLDLSLVQXGVVSCQOVNTDSETA 120  
Db 61 IELHCKPIEVEHSVKKRQRIKRLQIRNIPHLQMEVLDLSLVQXGVVSCQOVNTDSETA 120  
QY 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGQRSS 180  
Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGQRSS 180  
QY 181 RQSPGVSYSKQPCDPLRLVLPTQFVGAIIKGGATIRNTKOTQSKIDVHKENAGAA 240  
Db 181 RQSPGVSYSKQPCDPLRLVLPTQFVGAIIKGGATIRNTKOTQSKIDVHKENAGAA 240  
QY 241 EKSTIILSTPEGTSAAKCSILEIMHKEADIKFTEEIPKILAHNNFVGRILGKEGRNLK 300  
Db 241 EKSTIILSTPEGTSAAKCSILEIMHKEADIKFTEEIPKILAHNNFVGRILGKEGRNLK 300  
QY 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360  
Db 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360

Db 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360  
QY 361 QAHILPGNLNMGLEFPPTSGMPPTSGPSAMTPPYPOFQSETEYVHOFTIPALSVGAI 420  
Db 361 QAHILPGNLNMGLEFPPTSGMPPTSGPSAMTPPYPOFQSETEYVHOFTIPALSVGAI 420  
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMTITGPPEAQFKAGRTIGKIEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMTITGPPEAQFKAGRTIGKIEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAGAVIGKGTYNELQNTSSAEVYVPDQTPDENDQVYVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAGAVIGKGTYNELQNTSSAEVYVPDQTPDENDQVYVKIT 540  
QY 541 GHFYACQVAORIKQ 554  
Db 541 GHFYACQVAORIKR 554

## RESULT 12

US-09-724-676-92916  
Sequence 92916 Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92916

Query Match 83.28; Score 2459.5; DB 5; Length 492;  
Best Local Similarity 85.0%; Pred. No. 9.4e-202;  
Matches 492; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

QY 1 MNKLYIGNLSENAAPSDESIFDKAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60  
Db 1 MNKLYIGNLSENAAPSDESIFDKAKIPVSGPFLVKTGYAFVDCPDSESMALKAIEALSGK 60  
QY 61 IELHCKPIEVEHSVKKRQRIKRLQIRNIPHLQMEVLDLSLVQXGVVSCQOVNTDSETA 120  
Db 61 IELHCKPIEVEHSVKKRQRIKRLQIRNIPHLQMEVLDLSLVQXGVVSCQOVNTDSETA 120  
QY 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGQRSS 180  
Db 121 VVNVYSSKDOARQALDKLNGFQLENFTLKVAIIPDEMAAQNPLQOPRGRGLGQRSS 180  
QY 181 RQSPGVSYSKQPCDPLRLVLPTQFVGAIIKGGATIRNTKOTQSKIDVHKENAGAA 240  
Db 181 RQSPGVSYSKQPCDPLRLVLPTQFVGAIIKGGATIRNTKOTQSKIDVHKENAGAA 240  
QY 241 EKSTIILSTPEGTSAAKCSILEIMHKEADIKFTEEIPKILAHNNFVGRILGKEGRNLK 300  
Db 241 EKSTIILSTPEGTSAAKCSILEIMHKEADIKFTEEIPKILAHNNFVGRILGKEGRNLK 300  
QY 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360  
Db 301 KIEODTDKTIITSPLOELTYNPERTIVKGNVETCAKAEELMKIRRESYENDIASMNL 360  
QY 361 QAHILPGNLNMGLEFPPTSGMPPTSGPSAMTPPYPOFQSETEYVHOFTIPALSVGAI 420  
Db 361 QAHILPGNLNMGLEFPPTSGMPPTSGPSAMTPPYPOFQSETEYVHOFTIPALSVGAI 420  
QY 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMTITGPPEAQFKAGRTIGKIEENFV 480  
Db 421 IKGOGHIKOLSRFAGASIKIAPAEAPDAKRVMTITGPPEAQFKAGRTIGKIEENFV 480

OY 481 SPKEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDENDQVVKIT 540  
 Db 467 ----- 466  
 OY 541 GHFYACQVAAQRKIOELITOVKHOQOKALQSGPQSRK 579  
 Db 467 -----GEILTVKHOQOKALQSGPQSRK 492

## RESULT 13

US-09-724-676A-92916  
 ; Sequence 92916, Application US/09724676A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Compugen LTD  
 ; TITLE OF INVENTION: Variants of alternative splicing  
 ; FILE REFERENCE: 129181.4 Compugen  
 ; CURRENT APPLICATION NUMBER: US/09/724,676A  
 ; CURRENT FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 97222  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 92916  
 ; LENGTH: 492  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-724-676A-92916

Query Match 83.2%; Score 2459.5; DB 5; Length 492;  
 Best Local Similarity 85.0%; Pred. No. 9,4e-202;  
 Matches 492; Conservative 0; Mismatches 0; Indels 87; Gaps 1;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
 Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
 OY 61 IELHGKPIEVESHVPRKQRIKRIKQIRNIPPHLOMEVLDLLOYGVYVSCQVNTDSEFA 120  
 Db 61 IELHGKPIEVESHVPRKQRIKRIKQIRNIPPHLOMEVLDLLOYGVYVSCQVNTDSEFA 120  
 OY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGQSGSS 180  
 Db 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGQSGSS 180  
 OY 122 VVNVTVSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGQSGSS 180  
 Db 122 VVNVTVSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGQSGSS 180  
 OY 181 RQSGPESVSKQPCDLPRLVPPQVGAIIKKGATIRNITKOTOSKIDVHKKENAGAA 240  
 Db 181 RQSGPESVSKQPCDLPRLVPPQVGAIIKKGATIRNITKOTOSKIDVHKKENAGAA 240  
 OY 241 EKSITILSTPEGSTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRILGEGRNLK 300  
 Db 241 EKSITILSTPEGSTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRILGEGRNLK 300  
 OY 301 KIEQOTDTKITTISPLQELITLYNPERTITVKGNAVETCAKAEELIMKIRRESEYENDIASMNL 360  
 Db 301 KIEQOTDTKITTISPLQELITLYNPERTITVKGNAVETCAKAEELIMKIRRESEYENDIASMNL 360  
 OY 361 QAHLLPGLNLNLGLFPPTSGMPPTSGPSPAMTPPYPOFEOSTETVHOFPALSVGAI 420  
 Db 361 QAHLLPGLNLNLGLFPPTSGMPPTSGPSPAMTPPYPOFEOSTETVHOFPALSVGAI 420  
 OY 421 IKGOGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKQAGRIYGIKREENV 480  
 Db 421 IKGOGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKQAGRIYGIKREENV 480  
 OY 481 SPKEVKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDENDQVVKIT 540  
 Db 467 ----- 466

OY 541 GHFYACQVAAQRKIOELITOVKHOQOKALQSGPQSRK 579  
 Db 467 -----GEILTVKHOQOKALQSGPQSRK 492

RESULT 14  
 US-10-313-986-500

; Sequence 500, Application US/10313986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Foy, Teresa M.  
 ; APPLICANT: McNabb, Andria  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tonglong  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.455C19  
 ; CURRENT APPLICATION NUMBER: US/10/313,986  
 ; CURRENT FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 560  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 500  
 ; LENGTH: 577  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-313-986-500

Query Match 74.1%; Score 2191; DB 6; Length 577;  
 Best Local Similarity 74.2%; Pred. No. 1.1e-178;  
 Matches 435; Conservative 61; Mismatches 74; Indels 16; Gaps 8;

OY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
 Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAVFVDCPDPSMALKAIEALSGK 60  
 OY 61 IELHGKPIEVESHVPRKQRIKRIKQIRNIPPHLOMEVLDLLOYGVYVSCQVNTDSEFA 120  
 Db 61 IELHGKPIEVESHVPRKQRIKRIKQIRNIPPHLOMEVLDLLOYGVYVSCQVNTDSEFA 120  
 OY 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGQSGSS 179  
 Db 121 VVNVTVSSKDOARQALDKLNGFOLNFTLKAVYIPDEMAAOQNPLOQPRGRGLGQSGSS 176  
 OY 180 SROGSP---GSYSKQPCDLPRLVPPQVGAIIKKGATIRNITKOTOSKIDVHKKEN 236  
 Db 177 PROGSPVAGAPAKQOQVDPRLVPPQVGAIIKKGATIRNITKOTOSKIDVHKKEN 236  
 OY 237 AGAERKSTILSTPEGSTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRILGEGRN 296  
 Db 237 AGAERKSTILSTPEGSTSAACKSILEIMHKEADIKFTEEIPKLILAHNNFVGRILGEGRN 296  
 OY 297 RNLKIBQDTDKITTISPLQELITLYNPERTITVKGNAVETCAKAEELIMKIRRESEYENDIA 356  
 Db 297 RNLKIBQDTDKITTISPLQELITLYNPERTITVKGNAVETCAKAEELIMKIRRESEYENDIA 356  
 OY 357 SMNLQAHLLPGLNLNLGLFPPTSGMPPTSGPSPAMTPPYPOFEOSTETVHOFPALSVGAI 413  
 Db 357 SMNLQAHLLPGLNLNLGLFPPTSGMPPTSGPSPAMTPPYPOFEOSTETVHOFPALSVGAI 413  
 OY 414 ALSVGAIIKKGOGHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKQAGRIYGIK 473  
 Db 414 AOVAVGAIIGKGOHITQOLSRFAGASIKITAPAPADAKRYMIIITGPPEAOFKQAGRIYGIK 473  
 OY 474 IKENFVSPKEEYKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDENDQVVKIT 533  
 Db 474 IKENFVSPKEEYKLEAHIRVPSFAGRVIGKGTYNELQNLSSAEVVPDPTDENDQVVKIT 533  
 OY 534 QVNVKITGHFYACQVAAQRKIOELITOVKHOQOKALQSGPQSRK 579  
 Db 534 QVNVKITGHFYACQVAAQRKIOELITOVKHOQOKALQSGPQSRK 577

RESULT 15  
 US-09-724-676-48617  
 ; Sequence 48617, Application US/09724676  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Compugen LTD  
 ; TITLE OF INVENTION: Variants of alternative splicing  
 ; FILE REFERENCE: 129181.4 Compugen  
 ; CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48617

LENGTH: 572  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-724-676-48617

Query Match 71.4%; Score 2112; DB 5; Length 572;  
Best Local Similarity 72.4%; Pred. No. 6,4e-172;

Matches 422; Conservative 62; Mismatches 81; Indels 18; Gaps 8;

```
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVGTGAFVDCPDDESMALKAIETALSGK 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MNKLYIGNLSESVTPADELKVFAEHKISYSGQFLVKSAGAFVDCPDDEHMAKAIETFGSK 60

QY 61 IEHAKPIEVHSVPRKRIRIKLOIRINPHLOMEYLDLSLVQGVVSCQVNTDSETA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 VELQGRLEIHSVPRKORSRKIQIRNIPQOLMEYLDLSLAQYGVVSCQVNTDSETA 120

QY 121 VVNVVYSSKDAQALDKLNGFQLENFTLKAVIPDEMAAOQNPLOQPRGR-GIGQGRS 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 VVNVVYSNREQTRQAIMKLNCHQLENHAKLVSYIPDEQIAQ---GPENGRRGFGSRCQ 176

QY 180 SRQ---GSPGSVSKQKPCDPLRLVLPVTFQVGAIGKEGATIRNITKOTOSKIDVHRKEN 236
    || || || || || || || || || || || || || || || || || || || || || || ||
DB 177 PRQVTCGS-GGPAKQOQVDPLRLVLPVTFQVGAIGKEGATIRNITKOTOSKIDVHRKEN 235

QY 237 AGAAEKSTILSTPEGTAAACKSLTEIMHKEADIKFTEIETPLKILAHNMFVGRLLIGREG 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 PGAAEKALSVHSTPEGCSSACKMLETIMHKEADIKFTEIETPLKILAHNMFVGRLLIGREG 295

QY 297 RNKLTIEDPTDKITITISPLQELTLVNEERTITVKGNETCAKAEETMKKIRSEYENDIA 356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 RNKLTKEQDTEKITITISPLQELTLVNEERTITVKGNETCAKAEETMKKIRSEYENDIA 355

QY 357 SMNLQAHLPGLNLNALGLFPPTSGMPPTSGPPSAMT--PPYPOFEQS-ETETVHQFIP 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 356 AMSLQSHLPGLNLNALGLFPASSAVP--PPSSVTGAPAYSSFMQAPEDQEMVQVFIIP 412

QY 414 ALSVGAITIGKOGHITKQISPRAGASIKINAPAEAPDAXYRMVITITGPPEAQFKAQGRITGK 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 413 AQAVGAILIKKQOHITKQISPRASASIKIAPKTPDSKYRMVILIDROAPQFKAQGRITGK 472

QY 474 IKENEFVSPKEEVKLEAHIRVPSFAGRVIGKGTIVNELONLSAEVVPVRODTPDEND 533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 473 LKEENFEGPKEEVKLETHIRVPASAGRVIGKGTIVNELONLTAEEVVPVRODTPDEND 532

QY 534 QVVVKITGHFYACQVAKRIQELITGVKHOQOKALOSGPPQS 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 533 QVIVKITIGHFYASQMAQRKIRIDILAQV--QOKSRVCSPPQA 572
```

Search completed: April 16, 2003, 16:31:17  
Job time : 72.3054 secs





XX Isolated polypeptide comprising an immunogenic portion of a lung tumor  
PT protein is used for detecting and monitoring progression of lung cancer  
in a patient -  
XX  
XX  
XX Claim 3; Page 186-188; 261pp; English.  
XX  
XX This invention describes a novel isolated polypeptide (1) which  
CC comprises an immunogenic portion of a lung tumor protein or variant (P2)  
CC which has cytostatic activity and is used to inhibit the development of  
CC used in compositions and vaccines to inhibit the development of lung  
CC especially lung cancer, in a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.  
XX  
XX Sequence 579 AA:  
SQ  
Query Match Best Local Similarity 100.0%; Score 19; DB 21; Length 579;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TGYAFVDCPDESMALKAE 19  
DB 37 TGYAFVDCPDESMALKAE 55  
RESULT 2  
AB11365  
ID AB11365 standard; Protein; 579 AA.  
XX  
XX AB11365:  
XX 21-FEB-2001 (first entry)  
XX  
XX Human lung cancer associated antigen L5235.  
XX  
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
XX vaccine; detection.  
XX  
XX Homo sapiens.  
XX  
XX MO200061612-AZ.  
XX  
XX 19-OCT-2000.  
XX  
XX 03-APR-2000; 2000MO-US08896.  
XX  
XX 02-APR-1999; 99US-0285479.  
XX 17-DEC-1999; 99US-0466396.  
XX 30-DEC-1999; 99US-0476496.  
XX 10-JAN-2000; 2000US-0480884.  
XX 22-FEB-2000; 2000US-0510376.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Fan L;  
XX WPI: 2000-628399/60.  
XX N-PSDB; AAC66035.  
XX  
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor  
PT protein is used for detecting and monitoring progression of lung cancer  
in a patient -  
XX  
XX Claim 3; Page 259-261; 261pp; English.  
XX  
XX This invention describes a novel isolated polypeptide (1) which  
CC comprises an immunogenic portion of a lung tumor protein or variant (P2)  
CC which have cytostatic activity. The polypeptides and polynucleotides are

CC used in compositions and vaccines to inhibit the development of cancer,  
CC especially lung cancer, in a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.  
XX  
XX Sequence 579 AA:  
SQ  
Query Match Best Local Similarity 100.0%; Score 19; DB 21; Length 579;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TGYAFVDCPDESMALKAE 19  
DB 37 TGYAFVDCPDESMALKAE 55  
RESULT 3  
AB174960  
ID AB174960 standard; Protein; 579 AA.  
XX  
XX AB174960:  
XX 01-MAY-2002 (first entry)  
XX  
XX Human lung tumour L5235 protein sequence SEQ ID NO:176.  
XX  
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
XX immune response.  
XX  
XX Homo sapiens.  
XX  
XX WO200200174-AZ.  
XX  
XX 03-JAN-2002.  
XX  
XX 28-JUN-2001; 2001WO-US21065.  
XX  
XX 28-JUN-2000; 2000US-0606421.  
XX 22-AUG-2000; 2000US-0619540.  
XX 21-SEP-2000; 2000US-0642786.  
XX 15-SEP-2000; 2000US-0662786.  
XX 09-OCT-2000; 2000US-0685696.  
XX 12-DEC-2000; 2000US-0735705.  
XX 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Wang A, Skelky YAM, Li SX, Kalos MD, Henderson RA;  
XX McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
XX Vevayick TS, Carter D, Watanabe Y, Peckham DW;  
XX WPI: 2002-090513/12.  
XX N-PSDB; ABL49119.  
XX  
XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Example 2; Page 267-268; 374pp; English.  
XX  
XX The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL48959 to ABL49300 and AB174946 to  
CC AB175070 represent sequences used in the exemplification of the present  
CC invention.

SQ Sequence 579 AA;

Query Match 100.0%; Score 19; DB 23; Length 579;

Best Local Similarity 100.0%; Pred. No. 2,1e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKATE 19

DB 37 TGYAFVDCPDESMALKATE 55

RESULT 4

ID ABB74997 standard; Protein; 579 AA.

AC ABB74997;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L5235 protein sequence SEQ ID NO:348.

KW Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KM immune response.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

XX 13-SEP-2000; 2000US-0662786.

XX 09-OCT-2000; 2000US-0685696.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

XX McKenill PD, Fanger N, Reiter MW, Marneakis M, Fanger GR;

XX Vedick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

XX N-PSDB; ABL49254.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

XX lung cancer or stimulating an immune response -

XX Example 2; Page 330-332; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

XX tumour proteins and polynucleotides have cytostatic and immunostimulant

XX activities, and can be used in vaccine production. Compositions

XX comprising the lung tumour proteins, polynucleotides, antibodies,

XX fusion proteins, T cell populations, or antigen presenting cells that

XX express the lung tumour proteins are useful for treating lung cancer or

XX stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

XX ABB75070 represent sequences used in the exemplification of the present

XX invention.

XX Sequence 579 AA;

OY 1 TGYAFVDCPDESMALKATE 19

DB 37 TGYAFVDCPDESMALKATE 55

RESULT 5

ID ABB75053 standard; Protein; 579 AA.

AC ABB75053;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L5235 recombinant protein sequence SEQ ID NO:446.

KW Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KM immune response.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

XX 15-SEP-2000; 2000US-0662786.

XX 09-OCT-2000; 2000US-0685696.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

XX McKenill PD, Fanger N, Reiter MW, Marneakis M, Fanger GR;

XX Vedick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

XX N-PSDB; ABL49297.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

XX lung cancer or stimulating an immune response -

XX Claim 2; Page 365-367; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

XX tumour proteins and polynucleotides have cytostatic and immunostimulant

XX activities, and can be used in vaccine production. Compositions

XX comprising the lung tumour proteins, polynucleotides, antibodies,

XX fusion proteins, T cell populations, or antigen presenting cells that

XX express the lung tumour proteins are useful for treating lung cancer or

XX stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

XX ABB75070 represent sequences used in the exemplification of the present

XX invention.

XX Sequence 579 AA;

OY 1 TGYAFVDCPDESMALKATE 19

DB 37 TGYAFVDCPDESMALKATE 55

RESULT 6

ID ABB75054 standard; Protein; 579 AA.

AC ABB75054;

DT 01-MAY-2002 (first entry)

```

XX Human Lung tumour L523S recombinant protein sequence SEQ ID NO:449.
DE
XX
XX Human; Lung tumour; Lung cancer; cytostatic; immunostimulant; vaccine;
KW Immune response.
XX
XX Homo sapiens.
OS
XX WO200200174-A2.
XX
XX 03-JAN-2002.
XX
XX 28-JUN-2001; 2001WO-US21065.
XX
XX 28-JUN-2000; 2000US-0606421.
XX
XX 02-AUG-2000; 2000US-0630940.
XX
XX 21-AUG-2000; 2000US-0643597.
XX
XX 15-SEP-2000; 2000US-0662786.
XX
XX 09-OCT-2000; 2000US-0685696.
XX
XX 12-DEC-2000; 2000US-0735705.
XX
XX 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
XX
XX N-PSDB; ABL49299.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response.
XX
XX Claim 2: Page 368-369; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL4959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 579 AA:
SQ
Query Match 100.0%; Score 19; DB 23; Length 579;
Best Local Similarity 100.0%; Pred. No. 2,le-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGYAFVDCPDSEWALKAIE 19
DB 37 TGYAFVDCPDSEWALKAIE 55

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XX 03-JAN-2002.
XX
XX 28-JUN-2001; 2001WO-US21065.
XX
XX 28-JUN-2000; 2000US-0606421.
XX
XX 02-AUG-2000; 2000US-0630940.
XX
XX 21-AUG-2000; 2000US-0643597.
XX
XX 15-SEP-2000; 2000US-0662786.
XX
XX 09-OCT-2000; 2000US-0685696.
XX
XX 12-DEC-2000; 2000US-0735705.
XX
XX 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
XX
XX N-PSDB; ABL49283.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response.
XX
XX Claim 2: Page 354-355; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL4959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 586 AA:
SQ
Query Match 100.0%; Score 19; DB 23; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,le-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGYAFVDCPDSEWALKAIE 19
DB 44 TGYAFVDCPDSEWALKAIE 62

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PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedrick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Claim 2; Page 168; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 18 AA;
SQ
Query Match 84.2%; Score 16; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGYAFVDCPDSEWALK 16
DB 1 TGYAFVDCPDSEWALK 16

RESULT 9
ABR75027
ID ABR75027 standard; Peptide; 20 AA.
XX
XX ABR75027;
XX
XX 01-MAY-2002 (first entry)
XX
XX Human lung tumour L523S peptide SEQ ID NO:400.
DE
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KM immune response.
XX
XX Homo sapiens.
OS
XX WO200200174-A2.
PN
XX 03-JAN-2002.
ED
XX 28-JUN-2001; 2001WO-US21065.
PE
XX 28-JUN-2000; 2000US-0606421.
XX
XX 02-AUG-2000; 2000US-0630940.
PR
XX 21-AUG-2000; 2000US-0643597.
PR
XX 15-SEP-2000; 2000US-0662786.
PR
XX 09-OCT-2000; 2000US-0685696.
PR
XX 12-DEC-2000; 2000US-0735705.
PR
XX 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedrick TS, Carter D, Watanabe Y, Peckham DW;
XX

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DR WPI: 2002-090513/12.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Claim 2; Page 348; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 20 AA;
SQ
Query Match 84.2%; Score 16; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 AFVDCPDSEWALKALE 19
DB 1 AFVDCPDSEWALKALE 16

RESULT 10
ABR75061
ID ABR75061 standard; Peptide; 20 AA.
XX
XX ABR75061;
XX
XX 01-MAY-2002 (first entry)
XX
XX Human lung tumour L523S epitope SEQ ID NO:457.
DE
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KM immune response.
XX
XX Homo sapiens.
OS
XX WO200200174-A2.
PN
XX 03-JAN-2002.
PD
XX 28-JUN-2001; 2001WO-US21065.
PE
XX 28-JUN-2000; 2000US-0606421.
XX
XX 02-AUG-2000; 2000US-0630940.
PR
XX 21-AUG-2000; 2000US-0643597.
PR
XX 15-SEP-2000; 2000US-0662786.
PR
XX 09-OCT-2000; 2000US-0685696.
PR
XX 12-DEC-2000; 2000US-0735705.
PR
XX 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedrick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Claim 2; Page 167; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions

```

CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. AB148959 to AB149300 and AB174946 to  
CC AB175070 represent sequences used in the exemplification of the present  
CC invention.

XX  
SQ Sequence 20 AA:  
Query Match 84.2%; Score 16; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 AFDVDCPDESMALKE 19  
DB 1 AFDVDCPDESMALKE 16

RESULT 11  
ABG21963  
ID ABG21963 standard; Protein; 619 AA.  
XX  
AC ABG21963;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #21954.  
XX  
KM Human: chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PE 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
XX  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PM Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI: 2001-619362/73.  
XX  
DR N-PSDB: AAS86150.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20: SEQ ID No 52322; 103pp; English.

XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridization probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (II) is useful in gene therapy techniques  
CC for assisting in the expression of genes. (I) is also useful for  
CC identifying expressed genes. (I) is also useful for identifying  
CC (II) is useful for generating antibodies against it and for  
CC quantitating a polypeptide in tissues as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human

CC diagnostic amino acid sequences of the invention  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification. The sequence was obtained in electronic format directly from WIPO.  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

XX  
SQ Sequence 619 AA:  
Query Match 78.9%; Score 15; DB 22; Length 619;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGTAFVDCPDESMAL 15  
DB 73 TGTAFVDCPDESMAL 87

RESULT 12  
ABR75026  
ID ABR75026 standard; Peptide; 20 AA.  
XX  
AC ABR75026;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human lung tumour 15236 peptide SEQ ID NO:399.  
XX  
XX  
KM Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
XX immune response.  
XX  
KM Homo sapiens.  
XX  
OS Homo sapiens.  
XX  
PN WO200200174-A2.  
XX  
PD 03-JAN-2002.  
XX  
PE 28-JUN-2001; 2001WO-US21065.  
XX  
PR 28-JUN-2000; 2000US-0606421.  
XX  
PR 02-AUG-2000; 2000US-0630940.  
XX  
PR 21-AUG-2000; 2000US-0643597.  
XX  
PR 15-SEP-2000; 2000US-0662786.  
XX  
PR 09-OCT-2000; 2000US-0685696.  
XX  
PR 12-DEC-2000; 2000US-0735705.  
XX  
PR 07-MAY-2001; 2001US-0850716.  
XX  
PA (CORI-) CORIAX CORP.  
XX  
PM Wang T, Wang A, Sheiky YAM, Li SX, Kalos MD, Henderson RA;  
XX McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
XX Vedvick JS, Carter D, Metanabe Y, Peckham DW;  
XX  
DR WPI: 2002-090513/12.  
XX  
PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response.  
XX  
PS Claim 2: Page 348; 374pp; English.

XX  
CC The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, antigen presenting cells, that  
CC stimulate an immune response. AB148959 to AB149300 and AB174946 to  
CC AB175070 represent sequences used in the exemplification of the present  
CC invention.

XX  
SQ Sequence 20 AA:  
Query Match 68.4%; Score 13; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAFVDCPDSEW 13  
 |||||  
 DB 8 TGAFVDCPDSEW 20

## RESULT 13

ABR75070  
 ID ABR75070 standard; Peptide; 11 AA.

AC ABR75070;  
 XX

DT 01-MAY-2002 (first entry)  
 XX

DE LS235 antigenic epitope SEQ ID NO:466.  
 XX

KM Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
 XX immune response.  
 XX

OS Homo sapiens.  
 XX

PM W0200200174-A2.  
 XX

PD 03-JAN-2002.  
 XX

PF 28-JUN-2001; 2001MO-US21065.  
 XX

PR 28-JUN-2000; 2000US-0606421.  
 XX

PR 02-AUG-2000; 2000US-0630940.  
 XX

PR 21-AUG-2000; 2000US-0643397.  
 XX

PR 15-SEP-2000; 2000US-0662786.  
 XX

PR 09-OCT-2000; 2000US-0685696.  
 XX

PR 12-DEC-2000; 2000US-0735705.  
 XX

PR 07-MAY-2001; 2001US-0850716.  
 XX

XX (CORI-) CORIXA CORP.  
 XX

XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;  
 XX McNeill PD, Fanger N, Reller MW, Marinakis M, Fanger GR;  
 XX Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
 XX

XX WPI: 2002-090513/12.  
 XX

XX DR N-PSDB: ABL49300.  
 XX

XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
 XX lung cancer or stimulating an immune response -  
 XX

XX Claim 2; Page 168; 374pp; English.  
 XX

XX The present invention describes human lung tumor proteins. Human lung  
 XX tumor proteins and polynucleotides have cytostatic and immunostimulant  
 XX activities, and can be used in vaccine production. Compositions  
 XX comprising the lung tumor proteins, polynucleotides, antibodies,  
 XX fusion proteins, T cell populations, or antigen presenting cells that  
 XX express the lung tumor proteins are useful for treating lung cancer or  
 XX stimulating an immune response. ABL49300 and ABR74946 to  
 XX ABR75070 represent sequences used in the exemplification of the present  
 XX invention.  
 XX

XX SQ Sequence 11 AA;  
 XX

XX Query Match 57.9%; Score 11; DB 23; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVDCPDSEWAL 15  
 |||||  
 DB 1 FVDCPDSEWAL 11

RESULT 14  
 ABR21961  
 ID ABR21961 standard; Protein; 209 AA.

XX ABR21961;  
 AC  
 XX 18-FEB-2002 (first entry)  
 DT  
 XX Novel human diagnostic protein #21952.  
 DE  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX

OS Homo sapiens.  
 XX

PM W0200175067-A2.  
 XX

PD 11-OCT-2001.  
 XX

PF 30-MAR-2001; 2001MO-US08631.  
 XX

PR 31-MAR-2000; 2000US-0540217.  
 XX

PR 23-AUG-2000; 2000US-0649167.  
 XX

PA (HYSE-) HYSBO INC.  
 XX

PI Drmanac RT, Liu C, Tang YT;  
 XX

DR WPI: 2001-639362/73.  
 XX

DR N-PSDB: AAS86148.  
 XX

XX New isolated polynucleotide and encoded polypeptides, useful in  
 XX diagnostics, forensics, gene mapping, identification of mutations  
 XX responsible for genetic disorders or other traits and to assess  
 XX biodiversity -  
 XX

XX Claim 20; SEQ ID NO 52320; 103pp; English.  
 XX

XX The invention relates to isolated polynucleotide (I) and  
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 XX and gene mapping, and in recombinant production of (II). The  
 XX polynucleotides are also used in diagnostics as expressed sequence tags  
 XX for identifying expressed genes. (I) is useful in gene therapy techniques  
 XX to restore normal activity of (II) or to treat disease states involving  
 XX (II). (II) is useful for generating antibodies against it, detecting or  
 XX quantitating a polypeptide in tissue, as molecular weight markers and as  
 XX a food supplement. (II) and its binding partners are useful in medical  
 XX imaging of sites expressing (II). (I) and (II) are useful for treating  
 XX disorders involving aberrant protein expression or biological activity.  
 XX The polypeptide and polynucleotide sequences have applications in  
 XX diagnostics, forensics, gene mapping, identification of mutations in  
 XX responsible for genetic disorders or other traits to assess biodiversity  
 XX and to produce other types of data and products dependent on DNA and  
 XX amino acid sequences. ABR0010-ABG30377 represent novel human  
 XX diagnostic amino acid sequences of the invention.  
 XX Note: The sequence data for this patent did not appear in the printed  
 XX specification, but was obtained in electronic format directly from WIPO  
 XX at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX

XX SQ Sequence 209 AA;  
 XX

XX Query Match 52.6%; Score 10; DB 22; Length 209;  
 XX Best Local Similarity 100.0%; Pred. No. 0.01;  
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVDCPDE 11  
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 DB 15 GYAFVDCPDE 24

RESULT 15  
 ABR12593  
 ID ABR12593 standard; Protein; 266 AA.  
 AC ABR12593;

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XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #12584.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0645167.
XX
Z1 (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
XX
DR N-PSDB: AAS76780.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20: SEQ ID No 42952; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in
XX mapping of sites expressed (I) and (II) are useful for
XX identifying and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG0377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 266 AA:
XX
XX Query Match 52.6%; Score 10; DB 22; Length 266;
XX Best local Similarity 100.0%; Pred No. 0.012;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2 GYAFVDCPDE 11  
|||||  
18 GYAFVDCPDE 27

Search completed: April 16, 2003, 16:34:36  
Job time : 5.36782 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:32:15 ; Search time 1.34154 Seconds  
(without alignments)  
416.711 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 19

Sequence: 1 TGAFVDCPDESMALKAIE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfill1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	579	US-09-643-597-176	Sequence 176, App
2	19	100.0	579	US-09-643-597-348	Sequence 348, App
3	10	52.6	577	US-09-261-855-2	Sequence 2, Appl
4	6	31.6	72	US-08-973-273-27	Sequence 27, Appl
5	6	31.6	80	US-07-881-075-10	Sequence 10, Appl
6	6	31.6	80	US-08-120-827-10	Sequence 10, Appl
7	6	31.6	80	US-08-478-675-10	Sequence 10, Appl
8	6	31.6	443	US-09-134-001C-3183	Sequence 10, Appl
9	6	31.6	461	US-09-134-001C-3821	Sequence 3821, Ap
10	5	26.3	8	US-08-902-623-3	Sequence 3, Appl
11	5	26.3	44	US-08-580-031A-22	Sequence 22, Appl
12	5	26.3	44	US-08-580-031A-23	Sequence 22, Appl
13	5	26.3	48	US-09-227-357-241	Sequence 241, Appl
14	5	26.3	50	US-08-580-031A-32	Sequence 32, Appl
15	5	26.3	87	US-09-227-357-544	Sequence 544, App
16	5	26.3	103	US-09-308-388-1	Sequence 1, Appl
17	5	26.3	105	US-08-965-056-52	Sequence 52, Appl
18	5	26.3	105	US-08-965-056-54	Sequence 54, Appl
19	5	26.3	122	US-08-477-451-36	Sequence 54, Appl
20	5	26.3	139	US-09-570-921-57	Sequence 57, Appl
21	5	26.3	158	US-08-356-397-4	Sequence 4, Appl
22	5	26.3	158	US-08-850-119-4	Sequence 4, Appl
23	5	26.3	158	US-09-098-900-1	Sequence 1, Appl
24	5	26.3	158	US-09-098-900-3	Sequence 1, Appl
25	5	26.3	158	US-08-806-877-1	Sequence 1, Appl
26	5	26.3	158	US-08-806-877-3	Sequence 3, Appl
27	5	26.3	187	US-08-493-071-16	Sequence 16, Appl

28	5	26.3	188	US-08-933-750C-39	Sequence 39, Appl
29	5	26.3	188	US-09-234-613-39	Sequence 39, Appl
30	5	26.3	204	US-08-965-056-106	Sequence 106, App
31	5	26.3	232	US-08-173-510B-84	Sequence 84, Appl
32	5	26.3	232	US-08-458-218-82	Sequence 82, Appl
33	5	26.3	232	US-08-450-497-84	Sequence 84, Appl
34	5	26.3	236	US-08-493-071-15	Sequence 15, Appl
35	5	26.3	253	US-09-180-109A-35	Sequence 35, Appl
36	5	26.3	254	US-09-180-109A-31	Sequence 31, Appl
37	5	26.3	259	US-08-997-080-98	Sequence 98, Appl
38	5	26.3	259	US-08-997-362-98	Sequence 98, Appl
39	5	26.3	259	US-08-873-970-98	Sequence 98, Appl
40	5	26.3	259	US-09-095-855-98	Sequence 98, Appl
41	5	26.3	259	US-09-324-542-98	Sequence 98, Appl
42	5	26.3	259	US-09-205-426-98	Sequence 98, Appl
43	5	26.3	257	US-08-965-056-38	Sequence 38, Appl
44	5	26.3	259	US-08-965-056-21	Sequence 21, Appl
45	5	26.3	277	US-08-690-457-5	Sequence 5, Appl

## ALIGNMENTS

```

RESULT 1
US-09-643-597-176
: Sequence 176, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ. ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-643-597-176

Query Match      100.0%; Score 19; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAFVDCPDESMALKAIE 19
Db      37 TGAFVDCPDESMALKAIE 55

RESULT 2
US-09-643-597-348
: Sequence 348, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.

```

APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-348

Query Match 100.0%; Score 19; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.9e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAAVDCPDSEWALKATE 19  
|||||

Db 37 TGAAVDCPDSEWALKATE 55

## RESULT 3

US-09-261-855-2  
Sequence 2, Application US/09261855A  
Patent No. 625055  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261,855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-2

Query Match 52.6%; Score 10; DB 4; Length 577;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVDCPDE 11  
|||||

Db 38 GYAFVDCPDE 47

## RESULT 4

US-08-973-273-27  
Sequence 27, Application US/08973273  
Patent No. 6140085  
GENERAL INFORMATION:  
APPLICANT: Dean, Caroline  
APPLICANT: MacKnight, Richard C  
APPLICANT: Bancroft, Ian  
APPLICANT: Lister, Clare K  
TITLE OF INVENTION: Genetic Control of Flowering  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vandervhe P.C.  
STREET: 1100 No. 6140085th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,273  
FILING DATE: 01-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01332  
FILING DATE: 03-JUN-1996  
PRIOR APPLICATION DATA: GB 9511196.9  
APPLICATION NUMBER: GB 9511196.9  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-29  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4100  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 72 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-973-273-27

Query Match 31.6%; Score 6; DB 4; Length 72;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVD 7  
|||||

Db 51 GYAFVD 56

## RESULT 5

US-07-881-075-10  
Sequence 10, Application US/07881075  
Patent No. 544149  
GENERAL INFORMATION:  
APPLICANT: KEENE, JACK D.  
APPLICANT: KING, PETER H.  
APPLICANT: LEVINE, TODD  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE  
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ORLON, SPIYAK, MCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,075  
FILING DATE: 19920511  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: ORLON, SPIYAK, MCLELLAND, MAIER & NEUSTADT,  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 714-154-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)866-2347  
TELEFAX: (703)866-2347  
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-07-881-075-10

Query Match 31.6%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVD 7  
|||||  
DB 42 GYAFVD 47

RESULT 6  
US-08-120-827-10  
Sequence 10, Application US/08120827  
Patent No. 5525495

GENERAL INFORMATION:  
APPLICANT: KEENE, JACK D.  
APPLICANT: KING, PETER H.  
APPLICANT: LEVINE, TODD  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE  
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS  
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
ADDRESS: 1755 Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/120,827  
FILING DATE: 15-SEP-1993

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5525495man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 714-158-0 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)413-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-120-827-10

Query Match 31.6%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVD 7  
|||||  
DB 42 GYAFVD 47

RESULT 7  
US-08-478-675-10

Sequence 10, Application US/08478675  
Patent No. 5773246

GENERAL INFORMATION:  
APPLICANT: KEENE, JACK D.  
APPLICANT: KING, PETER H.  
APPLICANT: LEVINE, TODD  
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE  
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS  
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
ADDRESS: 1755 Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,675  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/120,827  
FILING DATE: 15-SEP-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5773246man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 714-158-0 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)413-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-478-675-10

Query Match 31.6%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYAFVD 7  
|||||  
DB 42 GYAFVD 47

RESULT 8  
US-09-134-001C-3183  
Sequence 3183, Application US/09134001C  
Patent No. 6380370

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3183  
LENGTH: 443

Thu Apr 17 07:55:18 2003

us-09-897-778-176\_copy\_37\_55.01igo.rai

Page 4

TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3183

Query Match 31.6%: Score 6; DB 4; Length 443;  
Best Local Similarity 100.0%: Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKATE 19  
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DB 258 ALKATE 263

RESULT 9  
US-09-134-001C-3821  
Sequence 3821, Application US/09134001C  
Patent No. 6380370

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3821  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3821

Query Match 31.6%: Score 6; DB 4; Length 461;  
Best Local Similarity 100.0%: Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFV 6  
|||||  
DB 252 TGYAFV 257

RESULT 10  
US-08-902-623-3  
Sequence 3, Application US/08902623  
Patent No. 5822345  
GENERAL INFORMATION:  
APPLICANT: MATTHEAKIS, LARRY C.  
APPLICANT: DOWER, WILLIAM J.  
TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY  
TITLE OF INVENTION: LIBRARIES  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,623  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/586,176  
FILING DATE: 17-JAN-1996

APPLICATION NUMBER: US 08/300,262  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/144,775  
FILING DATE: US 29-OCT-1993  
PRIOR APPLICATION DATA: PCT/US94/12206  
APPLICATION NUMBER: PCT/US94/12206  
FILING DATE: US 25-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: DUNN, TRACY J.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 16528X-003230US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-902-623-3

Query Match 26.3%: Score 5; DB 2; Length 8;  
Best Local Similarity 100.0%: Pred. No. 2e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFV 6  
|||||  
DB 2 GYAFV 6

RESULT 11  
US-08-580-031A-22  
Sequence 22, Application US/08580031A  
Patent No. 6428977  
GENERAL INFORMATION:  
APPLICANT: Graff, Jonathan M.  
APPLICANT: Wolff, Tod M.  
APPLICANT: Jin, Ping  
APPLICANT: Melton, Douglas A.  
TITLE OF INVENTION: The "signalin" Family of TcPb Signal  
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Eliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,031A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: ONV-019,01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)832-1000  
TELEFAX: (617)832-7000  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-580-031A-22

Query Match 26.3%; Score 5; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKAIE 19  
DB 27 LKAIE 31

RESULT 12  
US-08-580-031A-23  
Sequence 23, Application US/08580031A  
Patent No. 6428977  
GENERAL INFORMATION:  
APPLICANT: Graff, Jonathan M.  
APPLICANT: Woolf, Tod M.  
APPLICANT: Jin, Ping  
APPLICANT: Melton, Douglas A.  
TITLE OF INVENTION: The "Signalin" Family of TGF $\beta$  Signal  
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,031A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: ONV-019,01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)832-1000  
TELEFAX: (617)832-7000  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-031A-23

Query Match 26.3%; Score 5; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKAIE 19  
DB 27 LKAIE 31

RESULT 13  
US-09-227-357-241  
Sequence 241, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357

CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 241  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Homo sapiens

Thu Apr 17 07:55:18 2003

us-09-897-778-176\_copy\_37\_55\_oligo.ra1

Page 6

FEATURE:  
NAME/KEY: SITE  
LOCATION: (48)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-227-357-241

Query Match 26.3%; Score 5; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SMLK 16  
DB 6 SMLK 10

RESULT 14  
US-08-580-031A-32  
Sequence 32, Application US/08580031A  
Patent No. 6428977  
GENERAL INFORMATION:  
APPLICANT: Graff, Jonathan M.  
APPLICANT: Woolf, Tod M.  
APPLICANT: Jin, Ping  
TITLE OF INVENTION: The "Signalin" Family of TGF $\beta$  Signal  
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Foley Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580,031A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: ONV-019.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)832-7000  
TELEFAX: (617)832-7000  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-580-031A-32

Query Match 26.3%; Score 5; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKAIE 19  
DB 33 LKAIE 37

RESULT 15  
US-09-227-357-544  
Sequence 544, Application US/09227357  
Patent No. 6542581

GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P20101  
CURRENT APPLICATION NUMBER: US/09/227,357  
EARLIER FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
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EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
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EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
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EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
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EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
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EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 544  
LENGTH: 87  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-227-357-544

Query Match 26.3%; Score 5; DB 4; length 87;  
Best Local Similarity 100.0%; Pred No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 46 SWALK 50

Search completed: April 16, 2003, 16:38:11  
Job time : 2.34154 secs





Thu Apr 17 07:55:18 2003

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Page 1

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:36:47 ; Search time 2.18391 Seconds

(without alignments)  
657.841 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Sequence: 1 TGYAFVDCPDSEWALKAIE 19

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Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 7561385 residues

Word size : 0

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database :

Published Applications AA: \*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB\_PEP: \*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP: \*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB\_PEP: \*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP: \*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB\_PEP: \*  
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9: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP: \*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB\_PEP: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	579	10	US-09-735-705-176 Sequence 176, App
2	19	100.0	579	10	US-09-735-705-348 Sequence 348, App
3	19	100.0	579	10	US-09-850-716A-176 Sequence 176, App
4	19	100.0	579	10	US-09-850-716A-348 Sequence 348, App
5	19	100.0	579	10	US-09-897-778-176 Sequence 176, App
6	19	100.0	579	10	US-09-897-778-348 Sequence 348, App
7	19	100.0	579	10	US-09-897-778-446 Sequence 446, App
8	19	100.0	579	10	US-09-897-778-446 Sequence 446, App
9	19	100.0	586	10	US-09-850-716A-427 Sequence 427, App
10	19	100.0	586	10	US-09-850-716A-427 Sequence 427, App
11	19	100.0	586	10	US-09-897-778-465 Sequence 465, App
12	19	100.0	586	10	US-09-897-778-465 Sequence 465, App
13	19	100.0	586	10	US-09-735-705-400 Sequence 400, App
14	19	100.0	586	10	US-09-735-705-400 Sequence 400, App
15	19	100.0	586	10	US-09-897-778-457 Sequence 457, App
16	19	100.0	586	10	US-09-897-778-457 Sequence 457, App
17	19	100.0	586	10	US-09-735-705-399 Sequence 399, App
18	19	100.0	586	10	US-09-735-705-399 Sequence 399, App
19	19	100.0	586	10	US-09-897-778-466 Sequence 466, App

20	10	52.6	577	10	US-09-873-637-2	Sequence 2, Appl1
21	6	31.6	20	10	US-09-735-705-401	Sequence 401, App
22	6	31.6	20	10	US-09-850-716A-401	Sequence 401, App
23	6	31.6	20	10	US-09-897-778-401	Sequence 401, App
24	6	31.6	178	9	US-09-895-913A-20	Sequence 20, Appl1
25	6	31.6	178	10	US-09-881-752A-124	Sequence 124, App
26	6	31.6	286	6	US-09-815-242-10309	Sequence 10309, A
27	6	31.6	287	10	US-09-815-242-13772	Sequence 13772, A
28	6	31.6	332	10	US-09-738-626-5678	Sequence 5678, App
29	6	31.6	435	10	US-09-815-242-5283	Sequence 5283, App
30	6	31.6	436	10	US-09-815-242-12600	Sequence 12600, A
31	6	31.6	436	10	US-09-815-242-12732	Sequence 12732, A
32	6	31.6	620	10	US-09-764-864-1116	Sequence 1116, App
33	5	26.3	10	9	US-09-880-748-2200	Sequence 2200, App
34	5	26.3	36	10	US-09-779-451-33	Sequence 33, Appl1
35	5	26.3	38	10	US-09-779-451-34	Sequence 34, Appl1
36	5	26.3	44	12	US-10-095-492-22	Sequence 22, Appl1
37	5	26.3	44	12	US-10-095-492-23	Sequence 23, Appl1
38	5	26.3	45	10	US-09-779-451-32	Sequence 32, Appl1
39	5	26.3	48	9	US-09-983-802-241	Sequence 241, App
40	5	26.3	50	12	US-10-095-492-32	Sequence 32, Appl1
41	5	26.3	54	10	US-09-764-860-549	Sequence 549, App
42	5	26.3	57	10	US-09-864-761-42064	Sequence 42064, A
43	5	26.3	68	9	US-10-078-770-142	Sequence 142, App
44	5	26.3	71	10	US-09-864-761-37078	Sequence 37078, A
45	5	26.3	77	9	US-10-078-770-152	Sequence 152, App

# ALIGNMENTS

RESULT 1  
US-09-735-705-176  
Sequence 176 Application US/09735705  
Parent NO. US2002053228A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Hongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Katos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Yajun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FASTSD for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-176  
Query Match 100.0% Score 19; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 9.5e-13;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGYAFVDCPDSEWALKAIE 19  
DB 37 TGYAFVDCPDSEWALKAIE 55  
RESULT 2  
US-09-735-705-348  
Sequence 348 Application US/09735705

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Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: US/09/735,705
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRN
: ORGANISM: Homo sapiens
US-09-735-705-348

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 3
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US2001015139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRN
: ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 4
US-09-850-716A-348
: Sequence 348, Application US/09850716A
: Patent No. US2001015139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.

Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: US/09/735,705
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRN
: ORGANISM: Homo sapiens
US-09-735-705-348

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 5
US-09-897-778-176
: Sequence 176, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vegdick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRN
: ORGANISM: Homo sapiens
US-09-897-778-176

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9,5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESMALKAIE 19
DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 6
US-09-897-778-348
: Sequence 348, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vegdick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDSEWALKATIE 19
   |||
Db 37 TGTAFTDCPDSEWALKATIE 55

RESULT 7
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDSEWALKATIE 19
   |||
Db 37 TGTAFTDCPDSEWALKATIE 55

RESULT 8
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

Query Match          100.0%; Score 19; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.5e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDSEWALKATIE 19
   |||
Db 37 TGTAFTDCPDSEWALKATIE 55

RESULT 9
US-09-850-716A-427
; Sequence 427, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kaio, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-427

Query Match          100.0%; Score 19; DB 10; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTDCPDSEWALKATIE 19
   |||
Db 44 TGTAFTDCPDSEWALKATIE 62

RESULT 10
US-09-897-778-427
; Sequence 427, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
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LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-427

Query Match 100.0%; Score 19; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 9,6e-13;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKATE 19  
|||||  
DB 44 TGYAFVDCPDSEWALKATE 62

RESULT 11  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnierakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 465  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-465

Query Match 84.2%; Score 16; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7,8e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALK 16  
|||||  
DB 1 TGYAFVDCPDSEWALK 16

RESULT 12  
US-09-735-705-400  
Sequence 400, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Ligu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Banour, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skelvy, Jasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-400

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8,5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDSEWALKATE 19  
|||||  
DB 1 AFVDCPDSEWALKATE 16

RESULT 13  
US-09-850-716A-400  
Sequence 400, Application US/09850716A  
Patent No. US2002015139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Reller, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8,5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDSEWALKATE 19  
|||||  
DB 1 AFVDCPDSEWALKATE 16

RESULT 14  
US-09-897-778-400  
Sequence 400, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnierakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-400

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDDESMAKAE 19  
|||||  
DB 1 AFVDCPDDESMAKAE 16

## RESULT 15

US-09-897-778-457  
; Sequence 457, Application US/09897778  
; Patent No. US20020147143A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fang, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-457

Query Match 84.2%; Score 16; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPDDESMAKAE 19  
|||||  
DB 1 AFVDCPDDESMAKAE 16

Search completed: April 16, 2003, 16:48:43  
Job time : 4.18391 secs



GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:34:47 : Search time 12.8851 Seconds  
(without alignments)  
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Title: US-09-897-778-176\_COPY\_37\_55

Sequence: 1 TGVAFVDCPDSEMAIKAE 19

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Word size: 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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27: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	100.0	579	PCT-US01-47576-176	Sequence 176, App
3	19	100.0	579	PCT-US01-47576-348	Sequence 348, App
4	19	100.0	579	PCT-US01-47576-446	Sequence 446, App
5	19	100.0	579	PCT-US01-47576-449	Sequence 449, App
6	19	100.0	579	US-09-466-396A-176	Sequence 176, App

7	19	100.0	579	US-09-476-466A-176	Sequence 176, App
8	19	100.0	579	US-09-480-884A-176	Sequence 176, App
9	19	100.0	579	US-09-510-376A-176	Sequence 176, App
10	19	100.0	579	US-09-542-615A-176	Sequence 176, App
11	19	100.0	579	US-09-542-615A-348	Sequence 348, App
12	19	100.0	579	US-09-606-421A-176	Sequence 176, App
13	19	100.0	579	US-09-606-421A-348	Sequence 348, App
14	19	100.0	579	US-09-606-421B-176	Sequence 176, App
15	19	100.0	579	US-09-606-421B-348	Sequence 348, App
16	19	100.0	579	US-09-630-940B-176	Sequence 176, App
17	19	100.0	579	US-09-630-940B-348	Sequence 348, App
18	19	100.0	579	US-09-662-786-176	Sequence 176, App
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24	19	100.0	579	US-09-791-537-49019	Sequence 49019, A
25	19	100.0	579	US-09-791-537-86130	Sequence 86130, A
26	19	100.0	579	US-09-850-716-176	Sequence 176, App
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32	19	100.0	579	US-09-897-778-446	Sequence 446, App
33	19	100.0	579	US-09-897-778-449	Sequence 449, App
34	19	100.0	579	US-10-007-700-176	Sequence 176, App
35	19	100.0	579	US-10-007-700-348	Sequence 348, App
36	19	100.0	579	US-10-007-700-446	Sequence 446, App
37	19	100.0	579	US-10-007-700-449	Sequence 449, App
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43	19	100.0	579	US-10-117-982-484	Sequence 484, App
44	19	100.0	579	US-10-117-982-488	Sequence 488, App
45	19	100.0	579	US-10-117-982-489	Sequence 489, App

# ALIGNMENTS

RESULT 1  
US-10-117-982-482  
Sequence 482, Application US/10117982  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: Fangier, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Mericle, Barbara  
APPLICANT: Spies, Gregory A.  
APPLICANT: Fan, Liang  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121, 455C18  
CURRENT APPLICATION NUMBER: US/10/117,982  
NUMBER OF SEQ ID NOS: 484  
SOFTWARE: PasteSeq for Windows Version 4.0  
SEQ ID NO 482  
LENGTH: 43  
TYPE: PRT  
ORIGIN: Homo sapiens  
US-10-117-982-482  
Query Match 100.0%, Score 19, DB 25, Length 43;





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: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Peckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 449
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US01-47576-449

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Query Match      100.0%; Score 19; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 6
US-09-466-396A-176
: Sequence 176, Application US/09466396A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45504
: CURRENT APPLICATION NUMBER: US/09/466,396A
: CURRENT FILING DATE: 1999-12-17
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-466-396A-176

```

```

Query Match      100.0%; Score 19; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 7
US-09-476-496A-176
: Sequence 176, Application US/09476496A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.

```

```

: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
: TITLE OF INVENTION: LUNG CANCER
: FILE REFERENCE: 210121.45505
: CURRENT APPLICATION NUMBER: US/09/476,496A
: CURRENT FILING DATE: 1999-12-30
: NUMBER OF SEQ ID NOS: 254
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-476-496A-176

```

```

Query Match      100.0%; Score 19; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 8
US-09-480-884A-176
: Sequence 176, Application US/09480884A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45506
: CURRENT APPLICATION NUMBER: US/09/480,884A
: CURRENT FILING DATE: 2001-08-27
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-480-884A-176

```

```

Query Match      100.0%; Score 19; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TGYAFVDCPDDESMALKAIE 19
Db 37 TGYAFVDCPDDESMALKAIE 55

```

```

RESULT 9
US-09-510-376A-176
: Sequence 176, Application US/09510376A
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.45507
: CURRENT APPLICATION NUMBER: US/09/510,376A
: CURRENT FILING DATE: 2001-08-21
: NUMBER OF SEQ ID NOS: 330
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens

```

US-09-510-376A-176

Query Match 100.0%; Score 19; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKAIE 19  
DB 37 TGYAFVDCPDSEWALKAIE 55

RESULT 10

US-09-542-615A-176  
Sequence 176, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fangen, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542.615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKAIE 19  
DB 37 TGYAFVDCPDSEWALKAIE 55

RESULT 11

US-09-542-615A-348  
Sequence 348, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fangen, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542.615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKAIE 19  
DB 37 TGYAFVDCPDSEWALKAIE 55

RESULT 12

US-09-606-421A-176  
Sequence 176, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fangen, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606.421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKAIE 19  
DB 37 TGYAFVDCPDSEWALKAIE 55

RESULT 13

US-09-606-421A-348  
Sequence 348, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fangen, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606.421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 100.0%; Score 19; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.3e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKAIE 19  
DB 37 TGYAFVDCPDSEWALKAIE 55

RESULT 14

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US-09-606-421B-176
; Sequence 176, Application US/09606421B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-176

Query Match          100.0%; Score 19; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAAVDCPDPSMALKAE 19
DB 37 TGAAVDCPDPSMALKAE 55

RESULT 15
US-09-606-421B-348
; Sequence 348, Application US/09606421B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-348

Query Match          100.0%; Score 19; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAAVDCPDPSMALKAE 19
DB 37 TGAAVDCPDPSMALKAE 55

Search completed: April 16, 2003, 16:45:12
Job time : 13.8851 secs
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2

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:35:32 ; Search time 3.93103 Seconds  
(without alignments)  
753.673 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 19

Sequence: 1 TGTAFVDCPDESMALKAIE 19

Scoring table:

OLIGO  
Gapop 60.0 , Capext 60.0

Searched: 705215 seqs, 155932251 residues

Word size : 0

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending Patents AA New:\*  
1: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
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7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	43	6 US-10-313-986-482	Sequence 482, App
2	19	100.0	134	5 US-09-724-676-92917	Sequence 92917, A
3	19	100.0	134	5 US-09-724-676A-92917	Sequence 92917, A
4	19	100.0	492	5 US-09-724-676-92916	Sequence 92916, A
5	19	100.0	492	5 US-09-724-676A-92916	Sequence 92916, A
6	19	100.0	558	5 US-09-724-676-92918	Sequence 92918, A
7	19	100.0	558	5 US-09-724-676A-92918	Sequence 92918, A
8	19	100.0	579	6 US-10-313-986-176	Sequence 176, App
9	19	100.0	579	6 US-10-313-986-348	Sequence 348, App
10	19	100.0	579	6 US-10-313-986-446	Sequence 446, App
11	19	100.0	579	6 US-10-313-986-449	Sequence 449, App
12	19	100.0	579	6 US-10-313-986-480	Sequence 480, App
13	19	100.0	579	6 US-10-313-986-484	Sequence 484, App
14	19	100.0	579	6 US-10-348-119-255	Sequence 255, App
15	19	100.0	586	6 US-10-313-986-427	Sequence 427, App
16	19	100.0	586	6 US-10-313-986-486	Sequence 486, App
17	19	100.0	586	6 US-10-313-986-485	Sequence 485, App
18	19	100.0	586	6 US-10-313-986-400	Sequence 400, App
19	19	100.0	586	6 US-10-313-986-457	Sequence 457, App
20	19	100.0	586	6 US-10-313-986-508	Sequence 508, App
21	19	100.0	586	6 US-10-313-986-399	Sequence 399, App
22	19	100.0	586	6 US-10-313-986-470	Sequence 470, App
23	19	100.0	586	6 US-10-313-986-507	Sequence 507, App
24	19	100.0	586	6 US-10-313-986-466	Sequence 466, App
25	19	100.0	586	6 US-10-313-986-467	Sequence 467, App
26	19	100.0	586	6 US-10-313-986-468	Sequence 468, App

27	10	52.6	572	5	US-09-724-676A-48617	Sequence 48617, A
28	10	52.6	572	5	US-09-724-676A-48618	Sequence 48618, A
29	10	52.6	577	6	US-10-313-986-500	Sequence 500, App
30	10	52.6	598	5	US-09-724-676-48616	Sequence 48616, A
31	10	52.6	598	5	US-09-724-676-48621	Sequence 48621, A
32	10	52.6	598	5	US-09-724-676A-48616	Sequence 48616, A
33	10	52.6	598	5	US-09-724-676A-48621	Sequence 48621, A
34	10	52.6	602	5	US-09-724-676-48619	Sequence 48619, A
35	10	52.6	602	5	US-09-724-676-48620	Sequence 48620, A
36	10	52.6	602	5	US-09-724-676A-48619	Sequence 48619, A
37	10	52.6	602	5	US-09-724-676A-48620	Sequence 48620, A
38	6	31.6	20	6	US-10-313-986-401	Sequence 401, App
39	6	31.6	20	6	US-10-313-986-509	Sequence 509, App
40	6	31.6	75	6	US-10-282-122A-51701	Sequence 51701, A
41	6	31.6	97	5	US-09-513-999C-7342	Sequence 7342, App
42	6	31.6	120	6	US-10-366-683-24880	Sequence 24880, A
43	6	31.6	124	6	US-10-369-493-15644	Sequence 15644, A
44	6	31.6	124	6	US-10-369-493-16019	Sequence 16019, A
45	6	31.6	153	6	US-10-389-566-765	Sequence 765, App

## ALIGNMENTS

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RESULT 1
US-10-313-986-482
; Sequence 482, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Malanabe, Yoshinhiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313, 986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 482
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-482

Query Match      100.0%; Score 19; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.2e-16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGTAFVDCPDESMALKAIE 19
Db      5 TGTAFVDCPDESMALKAIE 23

RESULT 2
US-09-724-676-92917
; Sequence 92917, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92917

Query Match      100.0%; Score 19; DB 5; Length 134;
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Thu Apr 17 07:55:18 2003

us-09-897-778-176\_copy\_37\_55.Oligo.rapn

Page 2

Best Local Similarity 100.0%; Pred. No. 2,5e-15;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
|||||

DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 3  
US-09-724-676A-92917  
Sequence 92917, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92917

Query Match  
Best Local Similarity 100.0%; Pred. No. 2,5e-15;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
|||||

DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 4  
US-09-724-676-92916  
Sequence 92916, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92916

Query Match  
Best Local Similarity 100.0%; Pred. No. 9e-15;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
|||||

DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 5  
US-09-724-676A-92916  
Sequence 92916, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92916  
LENGTH: 492

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92916

Query Match  
Best Local Similarity 100.0%; Pred. No. 9e-15;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
|||||

DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 6  
US-09-724-676-92918  
Sequence 92918, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92918

Query Match  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
|||||

DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 7  
US-09-724-676A-92918  
Sequence 92918, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92918

Query Match  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMALKAIE 19  
|||||

DB 37 TGYAFVDCPDESMALKAIE 55

RESULT 8  
US-10-318-986-176  
Sequence 176, Application US/10313986  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

```

; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

RESULT 9
Query Match      100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TGYAFVDCPDDESMALKATE 19
        |||
Db      37 TGYAFVDCPDDESMALKATE 55

RESULT 9
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

Query Match      100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TGYAFVDCPDDESMALKATE 19
        |||
Db      37 TGYAFVDCPDDESMALKATE 55

RESULT 10
US-10-313-986-446
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-446
```

```

; ORGANISM: Homo sapiens
US-10-313-986-446

Query Match      100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TGYAFVDCPDDESMALKATE 19
        |||
Db      37 TGYAFVDCPDDESMALKATE 55

RESULT 11
US-10-313-986-449
; Sequence 449, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-449

Query Match      100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TGYAFVDCPDDESMALKATE 19
        |||
Db      37 TGYAFVDCPDDESMALKATE 55

RESULT 12
US-10-313-986-480
; Sequence 480, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-480

Query Match      100.0%; Score 19; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TGYAFVDCPDDESMALKATE 19
        |||
Db      37 TGYAFVDCPDDESMALKATE 55
```

```
RESULT 13
US-10-313-986-484
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 484
; LENGTH: 579
; TYPE: PRT
; ORGANISM: primate
US-10-313-986-484

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 579;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDPSWALKAIE 19
Db 37 TGYAFVDCPDPSWALKAIE 55

RESULT 14
US-10-348-119-255
; Sequence 255, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348.119
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 255
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-119-255

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 579;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDPSWALKAIE 19
Db 37 TGYAFVDCPDPSWALKAIE 55

RESULT 15
US-10-313-986-427
; Sequence 427, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
```

```
FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-427

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 586;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDPSWALKAIE 19
Db 44 TGYAFVDCPDPSWALKAIE 62

Search completed: April 16, 2003, 16:47:25
Job time : 4.93103 secs
```



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:31:34 ; Search time 1.21675 Seconds  
(without alignments)  
1501.176 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 19

Sequence: 1 TGTATVDCPDPSNALKATE 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

P1R\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.8	7	310	2	T44857
2	36.8	7	337	2	T30601
3	36.8	7	404	2	R39097
4	31.6	6	75	2	G37116
5	31.6	6	147	2	H86686
6	31.6	6	156	2	H84251
7	31.6	6	178	2	E71915
8	31.6	6	178	2	B64599
9	31.6	6	188	2	R83842
10	31.6	6	222	2	T47768
11	31.6	6	234	2	A12709
12	31.6	6	234	2	B97492
13	31.6	6	257	2	D69877
14	31.6	6	264	2	H97700
15	31.6	6	286	2	F90525
16	31.6	6	286	2	F65104
17	31.6	6	286	2	C91132
18	31.6	6	286	2	F85977
19	31.6	6	287	2	AC0899
20	31.6	6	313	2	G84335
21	31.6	6	318	2	B36972
22	31.6	6	318	2	S33433
23	31.6	6	319	2	T26450
24	31.6	6	324	2	D81452
25	31.6	6	340	2	C55070
26	31.6	6	340	2	UJ0292
27	31.6	6	340	2	T14921
28	31.6	6	354	2	R71312
29	31.6	6	354	2	B31639

30	31.6	366	2	B39725	sex-lethal sex det
31	31.6	367	2	A83825	peptidoglycan acet
32	31.6	377	2	C69955	peptidoglycan acet
33	31.6	397	2	T27950	hypothetical prote
34	31.6	399	2	S75862	translation elonga
35	31.6	436	2	C89926	hypothetical prote
36	31.6	450	2	E71909	hypothetical prote
37	31.6	460	2	G84246	phosphomannomutase
38	31.6	586	2	AD2493	hypothetical prote
39	31.6	620	2	B64379	hypothetical prote
40	31.6	749	2	G97782	hypothetical prote
41	31.6	770	2	A12421	hypothetical prote
42	31.6	47	2	T37086	probable IS elemen
43	26.3	59	2	C72203	hypothetical prote
44	26.3	65	2	H95007	hypothetical prote
45	26.3	68	2	S60688	env protein - huma

## ALIGNMENTS

RESULT 1  
T44857  
Probable hydroxylase d [imported] - Amycolatopsis orientalis (fragment)  
C:Species: Amycolatopsis orientalis  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 16-Feb-2001  
C:Accession: T44857  
R:Solenderg, P.J.; Matsushima, P.; Stack, D.R.; Wilkie, S.C.; Thompson, R.C.; Baltz, submitted to the EMBL Data Library, January 1997  
A:Description: Production of hybrid glycopeptide antibiotics in vitro and in strepto  
A:Reference number: 222861  
A:Accession: T44857  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-310 <SOL>  
A:Cross-references: EMBL:U84350; PIDN:AA849296.1  
A:Experimental source: strain C329.4  
A:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology  
F:146-282/Domain: cytochrome P450 homology <P45>

Query Match  
Best Local Similarity 100.0%; Pred. No. 2; 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPD 10  
DB 298 AFVDCPD 304

RESULT 2  
T30601  
Cytochrome P450 hydroxylase homolog PCZA361.27 - Amycolatopsis orientalis (fragment)  
N:Alternate names: PCZA361.27  
C:Species: Amycolatopsis orientalis  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 16-Feb-2001  
C:Accession: T30601  
R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard Chem. Biol. 3, 155-162, 1998  
A:Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin  
A:Reference number: 218804  
A:Accession: T30601  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-337 <VAN>  
A:Cross-references: EMBL:AJ223998  
F:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology  
F:173-309/Domain: cytochrome P450 homology <P45>

Query Match  
Best Local Similarity 36.8%; Score 7; DB 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AFVDCPD 10

DB 325 AFVDCPD 331

## RESULT 3

hypothetical protein PX01-54 - Bacillus anthracis virulence plasmid PX01  
C:Species: Bacillus anthracis  
C>Date: 12-Nov-1999 #sequence, revision 12-Nov-1999 #text, change 11-May-2000  
C:Accession: F59097  
R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Kellm, P.; Koehler  
J. Bacteriol. 181, 6509-6515, 1999  
A:Title: Sequence and organization of PX01, the large Bacillus anthracis plasmid harbored  
A:Reference number: A59091; MUID:99445483; PMID:10515943  
A:Accession: F59097  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1404 <KOR>  
A:Cross-references: GB:AE065404; NID:94894216; PIDN:ADJ3258.1; PID:94894270  
A:Experimental source: strain Sterne  
A:Note: similar to S-layer precursor, surface layer protein (814 aa). B. anthracis (p490)  
C:Genetics:  
A:Gene: PX01-54  
A:Genome: plasmid

## Query Match

Best Local Similarity 36.8%; Score 7; DB 2; Length 404;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SWALKAI 18  
DB 175 SWALKAI 181

## RESULT 4

probable nucleic acid binding protein, containing KH domain [imported] - Clostridium acet  
C:Species: Clostridium acetobutylicum  
C>Date: 12-Sep-2001 #sequence, revision 14-Sep-2001 #text, change 17-May-2002  
C:Accession: AF67116  
R:Nojima, J.; Breton, G.; Omelchenko, M.V.; Markarov, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium CLO  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: G97116  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-75 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK79722.1; PID:915024725; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1756  
C:Superfamily: Bacillus conserved hypothetical protein y1qc

## Query Match

Best Local Similarity 31.6%; Score 6; DB 2; Length 75;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 VCPDPE 11  
DB 13 VCPDPE 18

## RESULT 5

hypothetical protein yfha [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C>Date: 23-Mar-2001 #sequence, revision 23-Mar-2001 #text, change 03-Aug-2001  
C:Accession: H86696  
R:Belcino, A.; Winkler, P.; Manger, S.; Jallion, O.; Malmgren, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: H86696  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-147 <STO>  
A:Cross-references: GB:AE005176; PID:912723466; PIDN:AAK04674.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yfha  
C:Superfamily: Escherichia coli hypothetical 16.4k protein (trfE-meta intergenic r

## Query Match

Best Local Similarity 31.6%; Score 6; DB 2; Length 147;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAI 19  
DB 47 ALKAI 52

## RESULT 6

flagella-related protein E [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C>Date: 02-Feb-2001 #sequence, revision 02-Feb-2001 #text, change 02-Feb-2001  
C:Accession: H84251  
R:Ng, W.V.; Kennedy, S.P.; Maharis, G.G.; Benquist, B.; Pan, M.; Shukla, H.D.; Lask  
J. Lehman, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; J  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: H84251  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-156 <STO>  
A:Cross-references: GB:AE004437; NID:910580512; PIDN:AMG19380.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: fapE

## Query Match

Best Local Similarity 31.6%; Score 6; DB 2; Length 156;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAI 19  
DB 97 ALKAI 102

## RESULT 7

hydrogenase maturation factor hyad [similarity] - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C>Date: 12-Feb-1999 #sequence, revision 12-Feb-1999 #text, change 02-Sep-2000  
C:Accession: E71915  
R:Lim, R.A.; Ling, L.S.-L.; Moll, D.T.; King, B.D.; Brown, E.D.; Dolg, P.C.; Smith, D  
Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p  
A:Reference number: A71800; MUID:99120557; PMID:9923682  
A:Accession: E71915  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-178 <ARN>  
A:Cross-references: GB:AE001490; GB:AE001439; NID:94155115; PIDN:AMD06149.1; PID:9415  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: hyad  
C:Superfamily: Escherichia coli hydrogenase-1 maturation factor hyad  
Query Match 31.6%; Score 6; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19

Db 144 ALKAIE 149

#### RESULT 8

B64599

hydrogenase maturation factor HP0634 [similarity] - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C>Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 02-Sep-2000

C:Accession: B64599

R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKen-  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.  
Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; PMID:97394467; PMID:9252185

A:Accession: B64599

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-178 <TOM>

A:Cross-references: GB:AE000577; GB:AE000511; NID:q2313747; PIDN:AA07694.1; PID:q231375

C:Superfamily: Escherichia coli hydrogenase-1 maturation factor hyad

#### Query Match

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19

Db 144 ALKAIE 149

#### RESULT 9

F83842

stage V sporulation protein AE spovAE [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C:Accession: F83842

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir-  
Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83842

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-188 <STO>

A:Cross-references: GB:AP001512; GB:BA000004; NID:q10174030; PIDN:BA05261.1; GSPDB:GN00

A:Experimental source: strain C-125

C:Genetics:

A:Gene: spovAE

#### Query Match

Best Local Similarity 100.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19

Db 16 ALKAIE 21

#### RESULT 10

T47768

hypothetical protein F2413.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 19-May-2000

C:Accession: T47768

R:Nyakatura, G.; Fartmann, B.; Daner, D.; Sterr, W.; Holland, R.; Welchselgartner, M.;  
submitted to the Protein Sequence Database, February 2000

A:Reference number: 224475

A:Accession: T47768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <NYA>

A:Cross-references: EMBL:AL138655

A:Experimental source: cultivar Columbia; BMC clone F2413

C:Genetics:

A:Map position: 3

A:Introns: 84/3; 143/3; 181/3

A>Note: F2413.160

C:Superfamily: DNA-directed RNA polymerase chain PPS5

#### Query Match

Best Local Similarity 100.0%; Pred. No. 25;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19

Db 128 ALKAIE 133

#### RESULT 11

A12709

branched-chain amino acid permease Atutl082 [imported] - Agrobacterium tumefaciens (st

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Mar-2002

C:Accession: A12709

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo-  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McCI  
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam-  
ster, E.W.

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: A12709

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAL42095.1; PID:q17739477; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atutl082

A:Map position: circular chromosome

C:Superfamily: hypothetical protein b2682

#### Query Match

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DESNAL 15

Db 113 DESNAL 118

#### RESULT 12

B97492

azic family protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 01-Mar-2002

C:Accession: B97492

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldm  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,  
Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: B97492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK86891.1; PID:q15156113; GSPDB:GN00169

C:Genetics:

A:Gene: AGR\_C\_2001  
A:Map position: circular chromosome  
C:Superfamily: hypothetical protein b2682

Query Match 31.6%; Score 6; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DESMAL 15  
Db 113 DESMAL 118

## RESULT 13

uroporphyrin-III C-methyltransferase homolog yind - Bacillus subtilis

C:Species: Bacillus subtilis  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: D69877

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertier  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier  
lech, J.; Harwood, C.R.; Henaui, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee  
Y., M.; Ogawa, K.; Ogilvara, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Salto, T.; Scanlon,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Salto, T.; Scanlon,  
A:Authors: Schlach, S.; Schreier, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
akuchl, M.; Tanakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zunsstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A65580; MUID:98044033; PMID:9384377

A:Accession: D69877  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-257 <KUN>  
A:Cross-references: GB:429112; GB:AL009126; NID:g2633902; PIDN:CAHL3435.1; PID:g2633934  
A:Experimental source: strain 168  
C:Genetics:

C:Superfamily: S-adenosyl-L-methionine uroporphyrinogen methyltransferase

Query Match 31.6%; Score 6; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19  
Db 21 ALKAIE 26

## RESULT 14

H97700 hypothetical protein lpxa [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 22-Oct-2001  
C:Accession: H97700

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R  
Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:1157893

A:Accession: H97700  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <KUR>  
A:Cross-references: GB:AE006914; PIDN:AAI02546.1; PID:g15619040; GSPDB:GN00173  
C:Genetics:  
A:Gene: lpxa  
C:Superfamily: UDP-N-acetylglucosamine acyltransferase

Query Match 31.6%; Score 6; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19  
Db 213 ALKAIE 218

## RESULT 15

fructose-bisphosphate aldolase [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
C:Accession: F90525

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer,  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p  
A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: F90525  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-286 <KUR>  
A:Cross-references: GB:AL445566; PID:g14089523; PIDN:CAC13283.1; GSPDB:GN00153  
A:Experimental source: strain UAB CTIP  
C:Genetics:  
A:Gene: MYP0\_1100  
C:Superfamily: fructose-bisphosphate aldolase II

Query Match 31.6%; Score 6; DB 2; Length 286;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKAIE 19  
Db 91 ALKAIE 96

Search completed: April 16, 2003, 16:37:39  
Job time : 3.21675 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:23:10 ; Search time 0.967159 Seconds

(without alignments)  
814.809 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 19  
Sequence: 1 TGYAFVDCPDESWALKAE 19

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	31.6	75	YH56_CIOAB	097196 clostridium
2	6	31.6	185	RRE_THERH	09x76 thermus the
3	6	31.6	264	LPXA_RICCN	092199 rickettsia
4	6	31.6	264	LPXA_RICCN	P32199 rickettsia
5	6	31.6	286	YRAL_ECOLI	P45528 escherichia
6	6	31.6	307	SXL_CHRRU	097018 chrysomya r
7	6	31.6	318	SOLR_CIOAB	P33746 clostridium
8	6	31.6	324	FABH_CAMJE	0991h1 campylobact
9	6	31.6	324	SXL_MUSDO	017310 musca domes
10	6	31.6	340	RECA_THERH	P48297 thermus the
11	6	31.6	348	SXL_CERCA	061374 ceratilis c
12	6	31.6	349	ISPG_CIOPE	P58667 clostridium
13	6	31.6	354	SXL_DROME	P19339 drosophila
14	6	31.6	354	SXL_DROSU	02468 drosophila
15	6	31.6	367	ISPG_BACHD	09x18 bacillus ha
16	6	31.6	377	ISPG_BACSD	P54482 bacillus su
17	6	31.6	399	EPNU_FERTS	050340 fevriobact
18	6	31.6	399	EPNU_SYNY3	P74227 synecocyst
19	6	31.6	620	1E12_HSV2	058051 methanococ
20	5	26.3	58	1E12_HSV2	P14345 herpes simp
21	5	26.3	88	RL37_CANAL	09p836 candida alb
22	5	26.3	92	RPOL_SULSO	0980K0 sulfolobus
23	5	26.3	96	RS20_THEMA	09x1Y7 thermotoga
24	5	26.3	101	RS14_CAUCR	09a8u0 caulobacter
25	5	26.3	101	RS14_RHITO	09a8u4 rhizobium l
26	5	26.3	107	HIS2_AGRIS	08u191 agrobacteri
27	5	26.3	112	Y13K_SSV1	P20220 sulfolobus
28	5	26.3	119	YBX4_YEAST	P38269 saccharomyc
29	5	26.3	129	PEPD4_YEAST	P53900 saccharomyc
30	5	26.3	133	Y54L_SYNY3	P72777 synecocyst
31	5	26.3	144	SODM_EPTST	P28762 epatretus
32	5	26.3	152	YUVS_BPHHV	P13004 lactococcus
33	5	26.3	157	ALIS2_HUMAN	P56377 h adapter-r

34	5	26.3	158	1	ALIS2_HUMAN	000382 h adapter-r
35	5	26.3	160	1	ALIS2_MOUSE	09db50 m adapter-r
36	5	26.3	160	1	HPPK_AQUAE	066550 aquifex aeo
37	5	26.3	160	1	HPPK_HAETN	P43777 haemophilus
38	5	26.3	174	1	ARF6_XENLA	P51645 xenopus lae
39	5	26.3	181	1	YNEA_BACSU	P42408 bacillus su
40	5	26.3	185	1	SYN4_XENLA	009004 xenopus lae
41	5	26.3	186	1	FINO_ECO57	082922 escherichia
42	5	26.3	186	1	FINO_ECOLI	P22707 escherichia
43	5	26.3	186	1	FI02_ECOLI	P08315 escherichia
44	5	26.3	186	1	FI03_ECOLI	P29367 escherichia
45	5	26.3	186	1	FI04_ECOLI	005781 escherichia

## ALIGNMENTS

RESULT 1	YH56_CIOAB	STANDARD;	PRT;	75 AA.
ID	YH56_CIOAB			
AC	097196;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hypothetical protein CAC1756.			
GN	CAC1756.			
OS	Clostridium acetobutylicum.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_Taxid=1488;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ATCC 824 / DSM 792 / VKM B-1787;			
RX	MEDLINE=21359325; PubMed=11466286;			
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,			
RA	Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf P.Y.I.,			
RA	Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,			
RA	Bennett G.N., Koonin E.V., Smith D.R.;			
RT	"Genome sequence and comparative analysis of the solvent-producing			
RT	Bacterium Clostridium acetobutylicum.";			
RT	J. Bacteriol. 183:4823-4838(2001).			
RL	J. Bacteriol. 183:4823-4838(2001).			
CC	1- SIMILARITY: BELONGS TO THE UPF0109 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; AB007684; AAK79722.1;			
DR	PROSITE; PS50084; KH_TYPE.1; FALSE NEG.			
KW	Hypochemical protein; RNA-binding; Complete proteome.			
FT	DOMAIN 29			
SO	SEQUENCE 75 AA; 8170 MW; A68E213FAFEZDE CRC64;			
	Query Match	31.6%;	Score 6;	DB 1;
	Best Local Similarity	100.0%;	Pred. No. 4.1;	Length 75;
	Matches 6;	Conservative	0;	Indels 0;
				Gaps 0;
QY	6 VDCPDE 11			
DB	13 VDCPDE 18			
RESULT 2	RRE_THERH	STANDARD;	PRT;	185 AA.
ID	RRE_THERH			
AC	09x76;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			

```
DE Ribosome recycling factor (Ribosome releasing factor) (RRF).
GN FRR.
OS Thermus thermophilus.
CC Bacteria: Thermus/Delnococcus group; Delnococci; Thermates;
OC Thermaceae; Thermus.
ON NCBI_TaxID=274;
RN [1]
RX MEDLINE=99229778; PubMed=10214965;
RA Fujimura T., Ito K., Nakayashiki T., Nakamura Y.;
RT "Number mutations in ribosome recycling factors of Escherichia coli and
RT Thermus thermophilus: evidence for C-terminal modulator element.";
RL FEBS Lett. 447:297-302(1999).
CC -1- FUNCTION: RESPONSIBLE FOR THE RELEASE OF RIBOSOMES FROM MESSENGER
CC RNA AT THE TERMINATION OF PROTEIN BIOSYNTHESIS. MAY INCREASE THE
CC EFFICIENCY OF TRANSLATION BY RECYCLING RIBOSOMES FROM ONE ROUND OF
CC TRANSLATION TO ANOTHER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RRF FAMILY.
CC -----
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CC -----
DR EMBL: AB016498; BAA76865.1;
DR HSPB: Q9X1B9; IDDS.
DR InterPro: IPR002861; RRF.
DR Pfam: PF01765; RRF; 1.
DR TIGRPFAM: TIGR00496; Irf; 1.
KW Protein biosynthesis.
SQ
SEQUENCE 185 AA; 20994 MW; F3135AEF7813328 CRC64;
Query Match 31.6%; Score 6; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 14 ALKAIE 19
Db 75 ALKAIE 80
RESULT 3
LPXA_RICCN STANDARD; PRT; 264 AA.
AC Q92309;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase
DE (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
GN LPXA OR RCO008.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
ON NCBI_TaxID=781;
RN [1]
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-F., Barbe V.,
RA Samon D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001)
CC -1- FUNCTION: Involved in the biosynthesis of lipid A, a
CC phosphorylated glycolipid that anchors the lipopolysaccharide to
CC the outer membrane of the cell (by similarity).
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
CC protein] + UDP-N-acetylglucosamine -> [acyl-carrier protein] +
CC
```

```
CC UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
CC -1- PATHWAY: Lipid A biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
CC LPXA SUBFAMILY.
CC -----
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CC -----
DR EMBL: AE008569; AL02546.1;
DR InterPro: IPR001431; Hexapep.-transf.
DR Pfam: PF00132; Hexapep. 7.
DR PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
KW transferase; Acyltransferase; Lipid A biosynthesis; Lipid synthesis;
KW Repeat; Complete proteome.
SQ
SEQUENCE 264 AA; 28513 MW; 0BF3119FC85D624 CRC64;
Query Match 31.6%; Score 6; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 14 ALKAIE 19
Db 213 ALKAIE 218
RESULT 4
LPXA_RICRI STANDARD; PRT; 264 AA.
AC P32199;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase
DE (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
GN LPXA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
ON NCBI_TaxID=783;
RN [1]
RX MEDLINE=94171066; PubMed=8125326;
RA Shaw E.I., Wood D.O.;
RT "Characterization of a Rickettsia rickettsii DNA fragment analogous
RT to the fir A-ORF17-LpxA region of Escherichia coli.";
RL Gene 140:109-113(1994).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
CC PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOPOLYSACCHARIDE TO
CC THE OUTER MEMBRANE OF THE CELL.
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
CC protein] + UDP-N-acetylglucosamine -> [acyl-carrier protein] +
CC UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
CC -1- PATHWAY: Lipid A biosynthesis; first step.
CC -1- SUBUNIT: HOMOTRIMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
CC LPXA SUBFAMILY.
CC -----
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CC -----
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DR EMBL: L22690: AAA26386.1: -  
DR HSSP: P10440: 1LXA.  
DR InterPro: IPR001451: Hexapep\_transf.  
DR Pfam: PF00132: hexapep: 7  
DR PROSITE: PS00101: HEXAPEP-TRANSFERASE; 1.  
DR Transferrase; Acyltransferase; Lipid A biosynthesis; Lipid synthesis;  
KW Repeat.  
SQ SEQUENCE 264 AA; 28333 MW; 7A24B38C76A596D0 CRC64;  
  
Query Match 31.6%; Score 6; DB 1; Length 264;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 14 ALKAIE 19  
DB 213 ALKAIE 218  
  
RESULT 5  
YRAL\_ECOLI STANDARD; PRT; 286 AA.  
AC P45528:  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein yral.  
GN YRAL OR B3146 OR Z4505 OR ECS4027.  
OS Escherichia coli, and  
OC Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562, 83334;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RA MEDLINE=9742617; PubMed=9278503;  
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;  
RA MEDLINE=21074935; PubMed=11206551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blatter F.R.;  
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";  
RL Nature 409:529-533(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-O157:H7 / RIMD 0509952;  
RA MEDLINE=2156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Tida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
RA Kudara S., Shibata T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22(2001).  
-1- SIMILARITY: BELONGS TO THE UPF0011 FAMILY. STRONG, TO H.INFLUENZAE  
H1654.  
-----  
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-----  
DR EMBL: U18997: AAA57949.1: -  
DR EMBL: AF000395: AAC76180.1: -  
DR EMBL: AE005543: AAG58282.1: -  
DR EMBL: AP002564: BAB37450.1: -  
DR EcoGene: EG12777: yral.  
DR InterPro: IPR000878; Cor/por\_Mettransf.  
DR InterPro: IPR000578; UPF0011.  
DR Pfam: PF00590: TP\_methylase; 1.  
DR TIGRFAMs: TIGR00096: UPF0011; 1.  
DR PROSITE: PS01296: UPF0011; 1.  
DR Hypothetical protein; Complete proteome.  
KW SEQUENCE 286 AA; 31348 MW; 886EA92858PB95C CRC64;  
  
Query Match 31.6%; Score 6; DB 1; Length 286;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 14 ALKAIE 19  
DB 155 ALKAIE 160  
  
RESULT 6  
SXL\_CHRRU STANDARD; PRT; 307 AA.  
ID SXL\_CHRRU  
AC O97018;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Sex-lethal protein homolog.  
GN SXL.  
OS Chrysomya rufifacies (Hairy maggot blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Oestroidea; Calliphoridae; Chrysomya.  
OX NCBI\_TaxID=45450;  
[1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=96029145; PubMed=7563134;  
RA Mueller-Holtkamp F.;  
RT "The Sex-lethal gene homologue in Chrysomya rufifacies is highly  
RL conserved in sequence and exon-intron organization.";  
RL J. Mol. Evol. 41:467-477(1995).  
CC -1- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX  
CC DETERMINATION.  
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).  
CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE PRODUCED BY  
CC SEX-INDEPENDENT ALTERNATIVE SPLICING.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN BOTH SEXES FROM THE ONSET OF THE  
CC CELLULAR BLASTODERM FORMATION THROUGHOUT DEVELOPMENT.  
CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.  
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DR EMBL: S79722: -; NOT\_ANNOTATED\_CDS.  
DR HSSP: P19339: ISXL.  
DR InterPro: IPR002343; Hud\_Sxl\_RNA.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF00076; rrm; 2.  
DR PRINTS: PR00961; HODSXRNA.  
DR SMART: SM00360; RRM; 2.  
DR PROSITE: PS50102; RRM; 2.  
DR PROSITE: PS00030; RRM\_RNP\_1; 1.

KW RNA-binding; Repeat; Nuclear protein; Alternative splicing.  
 FT DOMAIN 85 163 RNA-BINDING (RRM) 1.  
 FT DOMAIN 171 251 RNA-BINDING (RRM) 2.  
 SQ SEQUENCE 307 AA: 33648 MW: 6F2C3DEFBF85B8FC CRC64:  
 Query Match 31.6%; Score 6; DB 1; Length 307;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GYAFVD 7  
 DB 127 GYAFVD 132  
 RESULT 7  
 SOLR\_CLOAB STANDARD; PRT: 318 AA.  
 ID SOLR\_CLOAB STANDARD; PRT: 318 AA.  
 AC P33746;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE SOL locus transcriptional repressor.  
 GN SOLR OR CAP0161.  
 OS Clostridium acetobutylicum.  
 OC Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE-94042861; PubMed-822639;  
 RA Fischer R.J., Helms J., Duerte P.;  
 RT "Cloning, sequencing, and molecular analysis of the sol operon of  
 Clostridium acetobutylicum, a chromosomal locus involved in  
 solventogenesis.";  
 RT J. Bacteriol. 175:6959-6969(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE-99084972; PubMed-9864345;  
 RA Nair R.V., Green E.M., Watson D.E., Bennett G.N., Papoutsakis E.T.;  
 RT "Regulation of the sol locus genes for butanol and acetone formation  
 in Clostridium acetobutylicum ATCC 824 by a putative transcriptional  
 repressor.";  
 RT J. Bacteriol. 181:319-330(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE-21359325; PubMed-1146286;  
 RA Neolling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng O.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,  
 RA Tatusov R.L., Sabatln E.V., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 bacterium Clostridium acetobutylicum.";  
 RT J. Bacteriol. 183:4823-4838(2001).  
 RL -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF THE SOL LOCUS (ADHE/AD,  
 CTFE, CTFB AND ADC) GENES FOR BUTANOL AND ACETONE FORMATION.  
 CC -1- SIMILARITY: CONTAINS 4 TPR REPEATS.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X72831; CA51342.1;  
 DR EMBL: L14817; ADO04637.1;  
 DR EMBL: AE001438; AAK76906.1;  
 DR PIR: S33433; S33433.

DR InterPro: IPR001440; TPR.  
 DR Pfam: PF00515; TPR; 5.  
 DR SMART: SM00028; TPR; 4.  
 KW Transcription regulation; Repressor; Repeat; TPR repeat; Plasmid;  
 KW Complete proteome.  
 FT REPEAT 65 98 TPR 1.  
 FT REPEAT 99 132 TPR 2.  
 FT REPEAT 133 166 TPR 3.  
 FT REPEAT 167 199 TPR 4.  
 SQ SEQUENCE 318 AA: 49CED287FEF4FEF8 CRC64:  
 Query Match 31.6%; Score 6; DB 1; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 ALKAIE 19  
 DB 223 ALKAIE 228  
 RESULT 8  
 FABH\_CAMJE STANDARD; PRT: 324 AA.  
 ID FABH\_CAMJE STANDARD; PRT: 324 AA.  
 AC Q9P1H1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41) (Beta-  
 ketoacyl-ACP synthase III) (KAS III).  
 GN FABH OR CJO328C.  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
 OC Campylobacter.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NCTC 11168;  
 RX MEDLINE-20150912; PubMed-10688204;  
 RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,  
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
 RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Pean C.W.,  
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,  
 RA Whitehead S., Barrett B.G.;  
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
 reveals hypervariable sequences.";  
 RT Nature 403:665-668(2000).  
 RL -1- FUNCTION: CATALYZES THE CONDENSATION REACTION OF FATTY ACID  
 SYNTHESIS BY THE ADDITION TO AN ACYL ACCEPTOR OF TWO CARBONS  
 FROM MALONYL-ACP. KAS III CATALYZES THE FIRST CONDENSATION  
 REACTION WHICH INITIATES FATTY ACID SYNTHESIS AND MAY THEREFORE  
 PLAY A ROLE IN GOVERNING THE TOTAL RATE OF FATTY ACID PRODUCTION.  
 CC POSSESSES BOTH ACETOACETYL-ACP SYNTHASE AND ACETYL TRANSACYLASE  
 ACTIVITIES (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-  
 carrier protein] = 3-oxoacyl-[acyl-carrier protein] + Co(2) +  
 [acyl-carrier protein].  
 CC -1- PATHWAY: Fatty acid biosynthesis.  
 CC -1- SIMILARITY: BELONGS TO THE FABH FAMILY.  
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 CC EMBL: AL139074; CAB72795.1;  
 DR HSSP: P24249; 1HNK.  
 DR InterPro: IPR004655; FABH.  
 DR InterPro: IPR001099; N-C-synthase.  
 DR Pfam: PF000453; N-C-synthase; 1.  
 DR TIGRfams: TIGR00747; fabh; 1.



KW Fatty acid biosynthesis; Transferase; Acyltransferase;  
 KM Multifunctional enzyme; Complete proteome;  
 FT ACT\_SITE 114 114 BY SIMILARITY.  
 FT ACT\_SITE 246 246 BY SIMILARITY.  
 FT ACT\_SITE 276 276 BY SIMILARITY.  
 SQ SEQUENCE 324 AA; 35165 MM; BIDE49F08016D9E CRC64;

Query Match 31.6%; Score 6; DB 1; Length 324;  
 Best local similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKATE 19  
 DB 60 ALKATE 65

## RESULT 9

SXL\_MUSDO STANDARD; PRT: 324 AA.  
 AC SXL\_MUSDO 017310; 017310;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sex-lethal protein homolog.  
 GN SXL.  
 OS Musca domestica (House fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Muscoidea; Muscidae; Musca.  
 OX NCBI\_TaxID=7370;  
 RN [1]  
 RC SEQUENCE FROM N.A. (ISOFORMS SXL1 AND SXL2).  
 RC TISSUE=Ovary;  
 RX MEDLINE=98171463; PubMed=9502729;  
 RA Melise M., Hilfler-Kleiner D., Duebendorfer A., Brunner C.,  
 RA Noehliger R., Bopp D.;  
 RT \*Sex-lethal, the master sex-determining gene in Drosophila, is not  
 RT sex-specifically regulated in Musca domestica.\*;  
 RL Development 125:1487-1494(1998).  
 CC -1- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX  
 CC DETERMINATION.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; SXL1 AND SXL2  
 CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SOMATIC CELLS OF BOTH SEXES  
 CC THROUGHOUT DEVELOPMENT, BUT NOT IN THE POLE CELLS WHICH ARE THE  
 CC PROGENITORS OF THE GERMLINE.  
 CC -1- DEVELOPMENTAL STAGE: FIRST APPEARS IN BLASTODERM EMBRYOS AFTER  
 CC ONSET OF CELLULARISATION.  
 CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
 CC -----  
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 CC -----  
 DR EMBL: AF025689; AAB81985.1; -;  
 DR EMBL: AF025690; AAB81986.1; -;  
 DR HSSP: P19339; 1SXL.  
 DR InterPro: IPR002343; Huo\_Sxl\_RNA.  
 DR InterPro: IPR000504; RNA\_rec-mot.  
 DR Pfam: PF00076; Rrm\_2.  
 DR PRINTS: PR00961; HODSXLRNA.  
 DR SMART: SM00360; RRM\_2.  
 DR PROSITE: PS50102; RRM\_2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
 KW RNA-binding; Repeat; Nuclear protein; Alternative splicing.  
 FT DOMAIN 102 180 RNA-BINDING (RRM) 1.  
 FT DOMAIN 188 268 RNA-BINDING (RRM) 2.  
 FT DOMAIN 88 94 POLY-GLY.

FT VANSPLIC 304 324 GRONKRNKHKVHPNPKKFI -> AYN5GLDGFYRNKS  
 FT CONFLICT 8 9 YHRYL (IN ISOFORM SXL1)  
 FT SEQUENCE 324 AA; 35755 MM; A65210EASCF67 CRC64;  
 SQ SEQUENCE 324 AA; 35755 MM; A65210EASCF67 CRC64;  
 Query Match 31.6%; Score 6; DB 1; Length 324;  
 Best local similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVD 7  
 DB 144 GYAFVD 149

## RESULT 10

RECA\_THERM STANDARD; PRT: 340 AA.  
 AC RECA\_THERM 09AG39;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE RecA protein (Recombinase A).  
 GN RECA.  
 OS Thermus thermophilus.  
 OC Bacteria; Thermus/Delnococcus group; Deinococci; Thermales;  
 OC Thermaceae; Thermus.  
 OX NCBI\_TaxID=274;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC MEDLINE=95014407; PubMed=7929298;  
 RA Wetmur J.G., Wong D.M., Ortiz B., Mong J., Reichert F., Gelfand D.H.,  
 RA Cloning, sequencing, and expression of RecA proteins from three  
 RT distantly related thermophilic bacteria.\*;  
 RL J. Biol. Chem. 269:25928-25931(1994).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=HB8 / ATCC 27634;  
 RX MEDLINE=94186518; PubMed=8138553;  
 RA Kato R., Kurimatsu S.;  
 RT \*RecA protein from an extremely thermophilic bacterium, Thermus  
 RT thermophilus HB8.\*;  
 RL J. Biochem. 114:926-929(1993).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=HB27;  
 RA Anasares L., Castan P., Barbe J., Berenguer J.;  
 RT \*Analysis of the Thermus thermophilus HB27 RecA.\*;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of  
 CC single-stranded DNA. The ATP-dependent uptake of single-stranded  
 CC DNA by duplex DNA, and the ATP-dependent hybridization of  
 CC homologous single-stranded DNAs. It interacts with LexA causing  
 CC its activation and leading to its autocatalytic cleavage.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U03058; AAA64935.1; -;  
 DR EMBL: D17392; BAA04215.1; -;  
 DR EMBL: AF318000; AAK13521.1; -;  
 DR HSSP: F26345; 1G19.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR001553; RecA.  
 DR Pfam: PF00154; RecA\_1.  
 DR PRINTS: PR00142; RECA.  
 DR ProDom: PD000229; RecA\_1.

DR SMART: SM00382; AAA: 1.  
DR PROSITE: PS00321; RECA\_1: 1.  
DR PROSITE: PS00162; RECA\_2: 1.  
DR PROSITE: PS00163; RECA\_3: 1.  
DR DNA damage: DNA recombination; SOS response; ATP-binding; DNA-binding.  
FM VARSPLIC 65 72  
FT BINDING 65 72  
FT CONFLICT 153 153  
FT CONFLICT 239 239  
FT CONFLICT 321 321  
FT CONFLICT 327 327  
SO SEQUENCE 340 AA; 36385 MW; 53F4A4A2F54B2BD4 CRC64;  
Query Match 31.6%; Score 6; DB 1; Length 340;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 14 ALKATE 19  
DB 12 ALKATE 17  
RESULT 11  
SXL\_CERCA STANDARD: PRT: 348 AA.  
ID SXL\_CERCA  
AC SXL\_CERCA  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Sex-lethal protein homolog (CCSXL).  
GN SXL.  
OS Ceratitis capitata (Mediterranean fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Tephritidae; Tephritidae; Ceratitis.  
OX NCBI\_TaxID=7213;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Benkelon; PubMed=9502730;  
RA Saccone G., Peluso I., Arliccio D., Giordano E., Bopp D., Pollito L.C.;  
RT The Ceratitis capitata homologue of the Drosophila sex-determining  
RT gene sex-lethal is structurally conserved, but not sex-specifically  
RT expressed.  
RL Development: 125-1495-1500(1998).  
CC -1- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX  
CC DETERMINATION.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS: ADULT-SPECIFIC ISOFORMS  
CC AL, AZ, A3, A4, AND EMBRYO-SPECIFIC ISOFORMS E1, E2 AND E3 (SHOWN  
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYOS OF BOTH SEXES. ALSO  
CC EXPRESSED IN THE PROGENITOR CELLS OF THE GERMLINE.  
CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
CC  
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CC  
CC EMBL: AF026145; AAC38966.1; -.  
CC HSSP: P19339; ISXL.  
DR InterPro: IPR000504; RNA\_rec\_mot.  
DR Pfam: PF00076; rrm; 2.  
DR SMART: SM00360; RRM; 2.  
DR PROSITE: PS00102; RRM; 2.  
DR PROSITE: PS00030; RRM\_RNP\_1; 1.  
KW RNA-binding; Repeat; Nuclear protein; Alternative splicing.  
FT DOMAIN 1 27  
FT DOMAIN 110 188 RNA-BINDING (RRM) 1.

FT DOMAIN 196 276 RNA-BINDING (RRM) 2.  
FT DOMAIN 68 75 POLY-GLY.  
FT DOMAIN 95 99 POLY-GLY.  
FT DOMAIN 293 311 POLY-GLY.  
FT DOMAIN 312 316 POLY-PRO.  
FT VARSPLIC 37 44  
SO SEQUENCE 348 AA; 37188 MW; CAB3D5C2C8B74A CRC64;  
Query Match 31.6%; Score 6; DB 1; Length 348;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 GYAFVD 7  
DB 152 GYAFVD 157  
RESULT 12  
ISPG\_CLOPE STANDARD: PRT: 349 AA.  
ID ISPG\_CLOPE  
AC P58667;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.  
DE 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.  
OS Clostridium perfringens.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium  
OX NCBI\_TaxID=1502;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=13 / Type A;  
RA PubMed=1192842;  
RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,  
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
RT flesh-eater".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
CC -1- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate  
CC (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate  
CC (by similarity).  
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway: sixth step.  
CC  
CC -1- SIMILARITY: BELONGS TO THE ISPG\_FAMILY.  
CC  
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CC  
CC EMBL: AF003191; BAB81398.1; -.  
CC InterPro: IPR004588; GCPE.  
DR InterPro: IPR000560; Nlr\_Sir.  
DR Pfam: PF01077; Nlr\_Sir; 1.  
DR TIGRPFAM: TIGR00612; gcpe; 1.  
KW Isoprene biosynthesis; Complete proteins.  
SO SEQUENCE 349 AA; 38017 MW; FC4B9508775BD343 CRC64;  
Query Match 31.6%; Score 6; DB 1; Length 349;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 14 ALKATE 19  
DB 88 ALKATE 93  
RESULT 13  
SXL\_DROME STANDARD: PRT: 354 AA.  
ID SXL\_DROME

AC P19339; P19340; Q99141; Q9TYF5; Q26466; Q9W3S6;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sex-lethal protein.  
 GN SXL OR SX1 OR CG18350.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS MS3 AND CM1).  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=89077532; PubMed=3144435;  
 RA Bell L.R., Maine E.M., Schedl P., Cline T.W.;  
 RT "Sex-lethal, a Drosophila sex determination switch gene, exhibits sex-  
 RT specific RNA splicing and sequence similarity to RNA binding  
 RT proteins.";  
 RL Cell 55:1037-1046(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS MS3; MS11 AND MS16).  
 RC TISSUE=Embryo;  
 RX MEDLINE=91260708; PubMed=1710769;  
 RA Samuels M.E., Schedl P., Cline T.W.;  
 RT "The complex set of late transcripts from the Drosophila sex  
 RT determination gene sex-lethal encodes multiple related  
 RT polypeptides.";  
 RL Mol. Cell. Biol. 11:3584-3602(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS MS3; MS11 AND CM1).  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G.G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,  
 RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
 RA Jaitai B., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Morkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-T., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [4]  
 RP SEQUENCE OF 1-26 FROM N.A. (ISOFORM EMBRYO-SPECIFIC).

RC TISSUE=Embryo;  
 RX MEDLINE=92191272; PubMed=1547493;  
 RA Keyes L.N., Cline T.W., Schedl P.;  
 RT "The primary sex determination signal of Drosophila acts at the level  
 RT of transcription.";  
 RL Cell 68:933-943(1992).  
 RN [5]  
 RP SEQUENCE OF 1-41 FROM N.A. (ISOFORM FEMALE-SPECIFIC).  
 RX MEDLINE=97132600; PubMed=8978052;  
 RA Penavalva L.O.F., Sakamoto H., Navarro-Sabate A., Sakashita E.,  
 RA Granadino B., Segarra C., Sanchez L.;  
 RT "Regulation of the gene Sex-lethal: a comparative analysis of  
 RT Drosophila melanogaster and Drosophila subobscura.";  
 RL Genetics 144:1653-1664(1996).  
 RN [6]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93087158; PubMed=1454517;  
 RA Sakamoto H., Inoue K., Higuchi I., Ono Y., Shimura Y.;  
 RT "Control of Drosophila Sex-lethal pre-mRNA splicing by its own female-  
 RT specific product.";  
 RL Nucleic Acids Res. 20:5533-5540(1992).  
 RN [7]  
 RP STRUCTURE BY NMR OF 199-294.  
 RX MEDLINE=95034815; PubMed=7524663;  
 RA Lee A.L., Kanaar R., Rio D.C., Wemmer D.E.;  
 RT "Resonance assignments and solution structure of the second  
 RT RNA-binding domain of sex-lethal determined by multidimensional  
 RT heteronuclear magnetic resonance.";  
 RL Biochemistry 33:13775-13786(1994).  
 RN [8]  
 RP STRUCTURE BY NMR OF 122-209.  
 RX MEDLINE=97446155; PubMed=9299339;  
 RA Inoue K., Muto Y., Sakamoto H., Kigawa T., Takio K., Shimura Y.,  
 RA Yokoyama S.;  
 RT "A characteristic arrangement of aromatic amino acid residues in the  
 RT solution structure of the amino-terminal RNA-binding domain of  
 RT Drosophila sex-lethal.";  
 RL J. Mol. Biol. 272:82-94(1997).  
 RN [9]  
 RP FUNCTION: SEX DETERMINATION SWITCH PROTEIN WHICH CONTROLS SEXUAL  
 RP DEVELOPMENT BY SEX-SPECIFIC SPLICING. REGULATES DOSAGE  
 RP COMPENSATION IN FEMALES BY SUPPRESSING HYPERACTIVATION OF X-LINKED  
 RP GENES. EXPRESSION OF THE EMBRYO-SPECIFIC ISOFORM IS UNDER THE  
 RP CONTROL OF X PRIMARY SEX-DETERMINING SIGNAL, WHICH DEPENDS ON THE  
 RP RATIO OF X CHROMOSOMES RELATIVE TO AUTOSOMES (X:A RATIO).  
 RP EXPRESSION OCCURS IN 2X:2A CELLS, BUT NOT IN X:2A CELLS. THE X:A  
 RP RATIO SEEMS TO BE SIGNALLED BY THE RELATIVE CONCENTRATION OF THE X-  
 RP LINKED TRANSCRIPTION FACTORS SIS-A AND SIS-B. AS A RESULT, THE  
 RP EMBRYO-SPECIFIC PRODUCT IS EXPRESSED EARLY ONLY IN FEMALE EMBRYOS  
 RP AND SPECIFIC FEMALE-ADULT SPECIFIC SPLICING; IN THE MALE WHERE IT  
 RP IS NOT EXPRESSED, THE DEFAULT SPLICING GIVES RISE TO A TRUNCATED  
 RP NONFUNCTIONAL PROTEIN. THE FEMALE-SPECIFIC ISOFORM SPECIFIES THE  
 RP SPLICING OF ITS OWN TRANSCRIPT, THEREBY INITIATING A POSITIVE  
 RP AUTOREGULATORY FEEDBACK LOOP LEADING TO FEMALE DEVELOPMENT  
 RP PATHWAY. THE FEMALE-SPECIFIC ISOFORM CONTROLS THE SEX-SPECIFIC  
 RP SPLICING OF TRANSFORMER (TRA); ACTS AS A TRANSLATIONAL REPRESSOR  
 RP FOR MALE-SPECIFIC LETHAL-2 (MSL-2) AND PREVENTS MALE-LESS (MLE),  
 RP MSL-1 AND MSL-3 PROTEINS FROM ASSOCIATING WITH THE FEMALE X  
 RP CHROMOSOME.  
 RN [10]  
 RP ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS: EMBRYO-SPECIFIC, MALE-  
 RP SPECIFIC CM1, FEMALE-SPECIFIC MS3/CF1 (SHOWN HERE), FEMALE-  
 RP SPECIFIC MS11 AND FEMALE-SPECIFIC MS16; ARE PRODUCED BY  
 RP ALTERNATIVE SPLICING.  
 RN [11]  
 RP TISSUE SPECIFICITY: EXPRESSED IN SOMATIC TISSUES, BUT NOT IN THE  
 RP POLE CELLS, WHICH ARE THE PRECURSORS OF THE GERMLINE.  
 RN [12]  
 RP DEVELOPMENTAL STAGE: THE EMBRYO-SPECIFIC ISOFORM IS EXPRESSED FOR  
 RP A BRIEF PERIOD DURING THE SYNCTIAL BLASTODERM STAGE. THE MALE-  
 RP SPECIFIC MS11 ISOFORM IS EXPRESSED IN 4-7 HOURS EMBRYO.  
 RN [13]  
 RP DOMAIN: THE GLY-ASN RICH DOMAIN IS REQUIRED FOR THE COOPERATIVE  
 RP INTERACTION WITH RNA AND FOR REGULATING THE SPLICING ACTIVITY.  
 RN [14]  
 RP SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).  
 RN [15]  
 RP This SWISS-PROT entry is copyright. It is produced through a collaboration  
 RP between the Swiss Institute of Bioinformatics and the EMBL outstation -



Search completed: April 16, 2003, 16:35:24  
 Job time : 5.96716 secs

```

FT DOMAIN 314 321 POLY-PRO.
FT VARSPLIC 1 25 MYGNNGSNNGGPPYGNKSS -> MDPSEYVTPPC
FT RPRGRITISRMQ (IN ISOFORM EMBRYO-
FT VARSPLIC 26 59 SPECIFIC).
FT GGRGFGMSHSLPSCGMSRYARSPDTEFSPPSSS -> SFH
FT SYGAGVTACPPSKSRNRRFRQKRTNRS (IN
FT ISOFORM MALE-SPECIFIC).
FT VARSPLIC 60 354 MISSING (IN ISOFORM MALE-SPECIFIC).
FT VARSPLIC 41 48 MISSING (IN SOME CLONES).
SO SEQUENCE 354 AA: 38715 MW: 760347AEF4DB7868 CRC64:

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Query Match 31.6%; Score 6; DB 1; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVD 7  
 |||||  
 Db 169 GYAFVD 174

```

RESULT 15
ISPG_BACHD STANDARD: PRT: 367 AA.
ID ISPG_BACHD
AC O9KD18:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase.
GN ISPG OR GCPE OR BH1401.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -i- FUNCTION: Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate
CC (ME-2,4cpP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC (by similarity).
CC -i- PATHWAY: Nonaevulonate terpenoid biosynthesis pathway; sixth step.
CC -i- SIMILARITY: BELONGS TO THE ISPG FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AP001511; BAB05120.1;
DR InterPro: IPR004588; GCPE.
DR InterPro: IPR000660; NIT_SIR.
DR Pfam: PF01077; NIT_SIR; 1.
DR TIGRFAMs: TIGR00612; gcpe; 1.
KW Isoprene biosynthesis; Complete proteome.
SO SEQUENCE 367 AA: 39581 MW: 217DD02965AMD2AD CRC64:

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Query Match 31.6%; Score 6; DB 1; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALKATE 19  
 |||||  
 Db 92 ALKATE 97



GenCore version 5.1.4-p5-4578  
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## OM protein - protein search, using sw model

Run on: April 16, 2003, 16:30:00 : Search time 2.3087 Seconds  
(without alignments)  
1695.712 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 19  
Sequence: 1 TGVAFVCPDESMALKATE 19

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_prodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	579	4	000425
2	11	57.9	100	11	09B054
3	11	57.9	579	11	09CPN8
4	10	52.6	576	13	042254
5	10	52.6	577	11	09N218
6	10	52.6	577	11	088477
7	10	52.6	582	13	09PW80
8	10	52.6	594	13	057526
9	10	52.6	594	13	073932
10	7	36.8	310	2	P96562
11	7	36.8	337	2	052816
12	7	36.8	404	2	09X324
13	7	36.8	406	2	087675
14	7	36.8	406	2	08RM03
15	7	36.8	653	5	09VX29
16	7	36.8	663	5	08STU3

17	6	31.6	114	10	09M455	09M455 elaeis guin
18	6	31.6	116	12	09MMY9	09MMY9 dioscorea a
19	6	31.6	147	16	09CH22	09CH22 lactococcus
20	6	31.6	156	17	09HQX2	09HQX2 halobacteri
21	6	31.6	178	16	025351	025351 helicobacte
22	6	31.6	178	16	09ZLK2	09ZLK2 helicobacte
23	6	31.6	188	16	09KCM7	09KCM7 bacillus ha
24	6	31.6	204	2	09F8C6	09F8C6 carboxydoth
25	6	31.6	222	10	09MJJ2	09MJJ2 arabidopsis
26	6	31.6	225	10	08S3U3	08S3U3 nicotiana b
27	6	31.6	234	16	08UGF6	08UGF6 agrobacteri
28	6	31.6	244	16	0981F4	0981F4 rhizobium l
29	6	31.6	250	16	08XOB0	08XOB0 raietonia s
30	6	31.6	257	16	034744	034744 bacillus su
31	6	31.6	268	2	09LCS2	09LCS2 azotobacter
32	6	31.6	286	16	09B8A0	09B8A0 mycoplasma
33	6	31.6	287	16	08Z1U5	08Z1U5 salmonella
34	6	31.6	287	16	08Z3U0	08Z3U0 salmonella
35	6	31.6	313	17	09HP19	09HP19 halobacteri
36	6	31.6	319	5	09U2W8	09U2W8 caenorhabdi
37	6	31.6	324	5	09BKK4	09BKK4 lucilia cup
38	6	31.6	325	5	09BKK3	09BKK3 lucilia cup
39	6	31.6	328	16	09ZSD9	09ZSD9 rhizobium m
40	6	31.6	340	16	09ZHL4	09ZHL4 yerstinia pe
41	6	31.0	342	3	0967U5	0967U5 cocciidiolde
42	6	31.0	344	16	0835S6	0835S6 tleponema p
43	6	31.0	374	17	08U205	08U205 pyrococcus
44	6	31.0	386	16	09XK16	09XK16 gliocetridium
45	6	31.6	387	5	023561	023561 caenorhabdi

## ALIGNMENTS

RESULT 1  
ID 000425 PRELIMINARY: PRT: 579 AA.  
AC 000425:  
DT 01-JUL-1997 (FIREBURL: 04, Created)  
DT 01-JUL-1997 (FIREBURL: 04, Last sequence update)  
DT 01-JUN-2002 (FIREBURL: 21, Last annotation update)  
DE Putative RNA binding protein KOC (KOC).  
GN KOC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mueller-Pillasch F., Lacher U., Wallrapp C., Et AL.:  
RL Oncogene 0:0-0(0).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANCREAS;  
RA Mueller-Pillasch F., Lacher U., Wallrapp C.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U76705; AAC3208.1; -  
DR EMBL: U76705; AAC09223.1; -  
DR InterPro: IPR004087; KH\_dom.  
DR InterPro: IPR004087; KH\_type\_1.  
DR InterPro: IPR005044; RNA\_rec\_mot.  
DR Pfam: PF00013; KH\_domain; 4.  
DR Pfam: PF00076; rim; 2.  
DR SMART: SM00322; KH; 4.  
DR SMART: SM00360; RRM; 2.  
DR PROSITE: PS50084; KH\_type\_1; 4.  
DR PROSITE: PS50102; RRM; 2.  
DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NRG.  
SQ SEQUENCE 579 AA; 63720 MW; AESC3ABEP3C135C5 CRC64;  
Query Match 100.0%; Score 19; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY	I	TGYAFVDCPDSESMALKATE	19
Dd	37	TGYAFVDCPDSESMALKATE	55
RESULT 2			
ID	09D054	PRELIMINARY:	PRT: 100 AA.
AC	09C054		
DT	01-JUN-2001	(TREMBLrel. 17, Created)	
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
GN	IGFZBP3 OR 261010INIRIK protein.		
DE	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sclerogamathi; Muridae; Eulestomii; Mus.		
RX	NCBI_TaxID=10090.		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;		
XC	MEDLINE=21085660; PubMed=11217851;		
RA	Araiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Alizawa K., Iwaza M., Nishl K., Kiyosawa H., Kondo S., Yamawaka I.,		
RA	Salto T., Okazaki Y., Gotojori T., Bono H., Kasakawa T., Salto R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Felschmann W., Gaasterland T., Gissi C., King B., Kochia H.,		
RA	Kuehl L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Oikido T., Furuno M., Anjo H., Balderas P., Bash G.,		
RA	Blahe A., Borrelli D., Bojunga N., Carrini P., de Bonis M.F.,		
RA	Garcia J., Hill D., Hofmeier C., Humedika M., Galipoli M.H.,		
RA	Guinichet S., Hill D., Hofmeier C., Humedika M., Galipoli M.H.,		
RA	Lyon P., Marchionni L., Maehina J., Mazzarelli J., Momberts P.,		
RA	Norione P., Ring B., Schonbach M., Seys T., Shibata Y., Storck K.-F.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storck K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Welz C., Whitaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Haasegawa Y., Kawaji H., Kohlski S.,		
RA	Hayashizaki Y. ;		
RT	"Functional annotation of a full-length mouse cDNA collection."		
RL	Nature 409:685-690(2001).		
DR	EMBL: AK011797; BAB27848.1; -		
DR	MGD: MGI:1890359.19T2B3.		
DR	PIR: F00078; F00078.O54; RNA_rec_mot.		
DR	SMART: SM00360; RM: 1		
DR	PROSITE: PSS0102; RM: 1.		
SO	SEQUENCE 100 AA; 11249 MW; 4DB71E37EB9D5466 CRC64;		
Query Match			
	Best Local Similarity	57.8%; Score 11; DB 11; Length 100;	
	Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;		
OY	I	TGYAFVDCPDE 11	
Dd	37	TGYAFVDCPDE 47	
RESULT 3			
ID	09C054	PRELIMINARY:	PRT: 579 AA.
AC	09C054		
DT	01-JUN-2001	(TREMBLrel. 17, Created)	
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	10 days embryo cDNA, RIKEN full-length enriched library,		
DE	clone:26100369b8r, full insert sequence (19f2 mRNA-binding protein		
DE	3).		
GN	IGFZBP3 OR 261010INIRIK OR MIMP3.		
OC	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;		

OC Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBT:TaxID=100950;  
 RN 11  
 RN SEQUENCE FROM N.A.  
 RP STRAIN: C57BL/6J; TISSUE=EMBRYO;  
 RP MEDIAN=21085660; PubMed=18117851;  
 RA Akiyama T., Hasegawa Y., Shikama K., Yoshino M., Itoh M., Ishii Y.,  
 RA Akiyama T., Hasegawa Y., Fukunishi Y., Kono H., Anaghi S., Yamada K.,  
 RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 RA Saito T., Matsuda Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Radocha K., Nakada H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischman W., Gaasterland T., Gliss C., King B., Koehle H.,  
 RA Kuehl P., Lewis S., Matsuno Y., Nikaido I., Plesing G., Quackenbush J.,  
 RA Schmal L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Oikido T., Furuno M., Aono H., Baladrelli R., Bash G.,  
 RA Blake J., Boilelli D., Bojunga N., Carinici P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gibson M.F.,  
 RA Cusack-Bennett S., Hall D., Holman M., Hume D.A., Kamita M., Lee R.H.,  
 RA Nguyen B.P., Richardson R.J., Matlma J., Mazzarelli S., Monodet S.F.,  
 RA Saeki K.H., Saito K., Schoenbach C., Seay T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyok-oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RA Mori H., Sakaibara S., Imai T., Nakamura Y., Iijima T., Suzuki A.,  
 RA Yuasa Y., Takena M., Okano T.,  
 RP Expression of mouse Igf2 mRNA-binding protein 3 and its implications  
 RP for the developing central nervous system.";  
 RP J. Neurosci. 19:1001-1011(1999).  
 RP PubMed: 10011689; PubMed327279.  
 DR EMBL: AK011689; BAB32729.1;  
 DR MGD: MGI:1890359; Igf2bp3.  
 DR InterPro: IPR004087; Igf2bp3.  
 DR InterPro: IPR004088; KH\_type.1.  
 DR InterPro: IPR005054; RNA\_rec\_mol.  
 DR Pfam: PF000013; KH-domain; 4.  
 DR Pfam: PF000076; rtm; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RM; 2.  
 DR PROSITE: PS20084; KH\_type.1; 4.  
 DR PROSITE: PS21022; RM; 2.  
 DR SEQUENCE 579 AA; 63574 MM; CABDPA4355832B7 CRC64;  
 QW Query Match 57.9%; Score 11; DA 11; length 579;  
 Db Best local similarity 100.0%; Pred. No. 0.001;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TGYAFVDCPDE 11  
 DB 37 TGYAFVDCPDE 47  
 RESULT 4  
 DA2254042354 PRELIMINARY: PRT: 576 AA.  
 AC 042254.  
 DT 01-JAN-1998 (TREMBLrel\_05, Created)  
 DT 01-JUN-1998 (TREMBLrel\_05, last sequence update)  
 DT 01-JAN-2002 (TREMBLrel\_21, last annotation update)  
 DE zipcode-binding protein.  
 GN zbp1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RL MEDLINE=97220007; PubMed=9121465;



RA Ross A.F., Oleynikov Y.S., Kislauskis E.H., Taneja K.L., Singer R.H.;  
 RT "Characterization of a beta-actin mRNA zipcode-binding protein.";  
 RL Mol. Cell. Biol. 17:2158-2165(1997).  
 DE EMBL: AF026527; AAB82295.1; -  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR005054; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PSS0030; RRM\_RNP\_1; FALSE\_NEG.  
 SQ SEQUENCE 576 AA: 63271 MW: 01AFA2D1D81C8811 CRC64:

Query Match 52.6%; Score 10; DB 13; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GYAFVDCPDE 11  
 |||||  
 Db 38 GYAFVDCPDE 47

## RESULT 5

09NZ18 PRELIMINARY; PRT; 577 AA.  
 AC 09NZ18;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE mRNA-binding protein CRDBP.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Ioannidis P., Trangas T., Dimitriadis E., Samiotaki M.,  
 RA Panoutsakopoulos G., Kyriazoglou I., Voutzoulis S., Tsilipalis C.M.,  
 RA Kittas C., Agnantis N., Pandis N.;  
 RT "Pectopic expression of a KH-domain containing protein, highly  
 RT homologous to both human IMP-1 and mouse CRD-BP, in benign and  
 RT malignant mesenchymal tumors.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF198254; AAF37203.1; -  
 DR HSSP: P11940; 1CVJ.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR005054; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; RRM; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PSS0084; KH\_type\_1; 4.  
 DR PROSITE: PSS0102; RRM; 2.  
 DR PROSITE: PSS0102; RRM; 2.  
 SQ SEQUENCE 577 AA: 63456 MW: 0749A060F252D81D CRC64:

Query Match 52.6%; Score 10; DB 4; Length 577;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GYAFVDCPDE 11  
 |||||  
 Db 38 GYAFVDCPDE 47

## RESULT 6

088477 PRELIMINARY; PRT; 577 AA.  
 AC 088477;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Coding region determinant binding protein (Coding region determinant-  
 DE binding protein).  
 GN tgf2bp1 OR CRDBP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92217743; PubMed=1559612;  
 RA Bernstein P.L., Herrick D.J., Prokipack R.D., Ross J.;  
 RT "Control of c-myc mRNA half-life in vitro by a protein capable of  
 RT binding to a coding region stability determinant.";  
 RL Genes Dev. 6:642-654(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94158886; PubMed=8114742;  
 RA Herrick D.J., Ross J.;  
 RT "The half-life of c-myc mRNA in growing and serum-stimulated cells:  
 RT influence of the coding and 3' untranslated regions and role of  
 RT ribosome translocation.";  
 RL Mol. Cell. Biol. 14:2119-2128(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94179348; PubMed=8132663;  
 RA Prokipack R.D., Herrick D.J., Ross J.;  
 RT "Purification and properties of a protein that binds to the C-terminal  
 RT coding region of human c-myc mRNA.";  
 RL J. Biol. Chem. 269:9261-9269(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97322234; PubMed=9178888;  
 RA Leeds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.,  
 RA Gruppuso P.A., Ross J.;  
 RT "Developmental regulation of CRD-BP, an RNA-binding protein that  
 RT stabilizes c-myc mRNA in vitro.";  
 RL Oncogene 14:1279-1286(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Ross J., Prokipack R.D., Leeds P., Doyle G.A.R., Betz N.A.,  
 RA Fleisig A.J.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,  
 RA Blake J., Botelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AF061569; AAC72743.1; -  
 DR EMBL: AK013940; BAB29071.1; -  
 DR HSSP: P11940; 1CVJ.  
 DR MGD: MGI:1890357; Igf2bp1.  
 DR InterPro: IPR004087; KH\_dom.

DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rim; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PS50084; KH\_type\_1; 4.  
 DR PROSITE: PS50102; RRM; 2.  
 SO SEQUENCE 577 AA; 63450 MW; EFBBIAPZFF9F0344 CRC64;

Query Match 52.6%; Score 10; DB 11; Length 577;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVDCPDE 11  
 DB 38 GYAFVDCPDE 47

## RESULT 7

ID O9PW80 PRELIMINARY; PRT; 582 AA.  
 AC O9PW80:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Vg1 RNA binding protein.  
 GN DRIHRB.  
 OC Brachydanio rerio (zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; 7955;  
 OC NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Q., Yaniv K., Oberman F., Wolke U., Git A., Fromer M.,  
 RA Taylor M., Meyer D., Standart N., Raz E., Yisraeli J.K.,  
 RT Vg1 RBP Intracellular distribution and evolutionarily conserved  
 RT expression suggest multiple roles during development.;  
 RL Mech. Dev. 0:0-0(1999).  
 RL EMBL: AF161270; A045610.1; -  
 RL ZFIN: ZDB-GENE-000308-1; dvrltbp.  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rim; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PS50084; KH\_type\_1; 4.  
 DR PROSITE: PS50102; RRM; 2.  
 SO SEQUENCE 582 AA; 63351 MW; 90AE63200681B306 CRC64;

Query Match 52.6%; Score 10; DB 13; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVDCPDE 11  
 DB 38 GYAFVDCPDE 47

## RESULT 8

ID O57526 PRELIMINARY; PRT; 593 AA.  
 AC O57526:  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE KH domain-containing transcription factor B3.  
 DE Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus.  
 OX NCBI\_Taxid=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-92249652; PubMed-1577195;  
 RX Pfaff S.L., Taylor W.L.;  
 RT "Characterization of a Xenopus oocyte factor that binds to a  
 RT developmentally regulated cis-element in the TfrII gene.";  
 RL Dev. Biol. 151:306-316(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Griffin D., Taylor W.L.;  
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RA Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,  
 RA Pressman Schwartz S., Standart N.M., Yisraeli J.K.;  
 RL Genes Dev. 0:0-0(1998).  
 DR EMBL: AF042353; AAB97457.1; -  
 DR EMBL: AF064633; AAC18597.1; -  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rim; 2.  
 DR SMART: SM00322; KH; 4.  
 DR SMART: SM00360; RRM; 2.  
 DR PROSITE: PS50084; KH\_type\_1; 4.  
 DR PROSITE: PS50102; RRM; 2.  
 DR PROSITE: PS00030; RRM\_RNP\_1; FALSE\_NEG.  
 SO SEQUENCE 593 AA; 65385 MW; 5A5AB4BA1D55DE7 CRC64;

Query Match 52.6%; Score 10; DB 13; Length 593;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVDCPDE 11  
 DB 38 GYAFVDCPDE 47

## RESULT 9

ID O73932 PRELIMINARY; PRT; 594 AA.  
 AC O73932:  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Vg1 RNA binding protein variant D.  
 DE Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_Taxid=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,  
 RA Pressman Schwartz S., Standart N.M., Yisraeli J.K.;  
 RL Genes Dev. 0:0-0(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-96228351; PubMed-9560341;  
 RX Deshler J.O., Hignett M.I., Abramson T., Schnapp B.J.;  
 RT "A highly conserved RNA-binding protein for cytoplasmic mRNA  
 RT localization in vertebrates.";  
 RL Curr. Biol. 8:469-496(1998).  
 DR EMBL: AF064634; AAC18598.1; -  
 DR EMBL: AF055923; AAC18597.1; -  
 DR InterPro: IPR004087; KH\_dom.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR Pfam: PF00013; KH-domain; 4.  
 DR Pfam: PF00076; rim; 2.

DR SMART: SM00322; KH: 4.  
 DR SMART: SM00360; RRM: 2.  
 DR PROSITE: PS50084; KH\_TYPE\_1: 4.  
 DR PROSITE: PS50102; RRM: 2.  
 SQ SEQUENCE 594 AA; 65643 MW; 54CEA7BFF0856DD6 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 10; DB 13; Length 594;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYAFVDCPD 11  
 DB 38 GYAFVDCPD 47

RESULT 10  
 P96562 PRELIMINARY; PRT; 310 AA.

AC P96562:  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Putative cytochrome P450 165C2 (Hypothetical hydroxylase D) (Fragment).  
 DE CYP165C2.  
 GN CYP165C2.  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C329.4;  
 RA Solenberg P.J., Matsushima P., Stack D.R., Wilkie S.C., Thompson R.C.,  
 RA Baltz R.H.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL: U84350; AAB49296.1; -  
 DR HSSP: 000441; 10XA;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450, UNKNOWN\_1.  
 KW Electron transport; Heme; Hypothetical protein; Membrane;  
 KW Monooxygenase; Oxidoreductase.  
 FT NON\_TER 1  
 FT BINDING 260 HEME (BY SIMILARITY)  
 SQ SEQUENCE 310 AA; 34255 MW; 0155572AP694487 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 310;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPD 10  
 DB 298 AFVDCPD 304

RESULT 11  
 O52816 PRELIMINARY; PRT; 337 AA.

AC 052816:  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE PC2A361.27 (Fragment).  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Wageningen A., Kirkpatrick P., Williams D., Harris B., Kershaw J.,  
 RA Leonard N., Jones M., Jones S., Solenberg P.;  
 RT \*Sequencing and analysis of genes involved in the biosynthesis of a

RT vancomycin group antibiotic.";  
 RL Chem. Biol. 3:155-162(1998).  
 CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL: AJ223998; CA11791.1; -  
 DR HSSP: 000441; 10XA.  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450, UNKNOWN\_1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 337 AA; 37418 MW; 75A3729A01C8CB89 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 337;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPD 10  
 DB 325 AFVDCPD 331

RESULT 12  
 O9X324 PRELIMINARY; PRT; 404 AA.

AC O9X324:  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PX01-54.  
 OS Bacillus anthracis.  
 OC Plasmid virulence plasmid PX01.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STERNE;  
 RL MEDLINE=99445483; PubMed=10515943;  
 RA Oklnaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.R.,  
 RA Kelm P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,  
 RA Martinez Y., Rieke D., Svensson R., Jackson P.J.;  
 RT "Sequence and organization of PX01, the large Bacillus anthracis  
 RT plasmid harboring the anthrax toxin genes.";  
 RL J. Bacteriol. 181:6509-6515(1999).  
 DR EMBL: AF065404; AAD32358.1; -  
 DR InterPro: IPR001119; SLH.  
 DR Pfam: PF00395; SLH.3.  
 DR PROSITE: PS01072; SLH\_DOMAIN; UNKNOWN\_1.  
 KW Plasmid.  
 SQ SEQUENCE 404 AA; 45044 MW; 45D08FAA450C0C4C CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 404;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SWALKAI 18  
 DB 175 SWALKAI 181

RESULT 13  
 O87675 PRELIMINARY; PRT; 406 AA.

AC 087675:  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Cytochrome P450 165C1 (Oxygenase C).  
 GN CYP165C1 OR OXYC.  
 OS Amycolatopsis mediterranei (Nocardia mediterranei).  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.  
 OX NCBI\_TaxID=33910;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DSM 5908;  
 RA Pelzer S., Suessmuth R., Heckmann D., Recktenwald J., Huber P.,  
 RA Jung G., Wohlleben W.;  
 RT Identification and analysis of a glycopeptide biosynthetic gene  
 RT cluster and its use for manipulating balhimycin biosynthesis in the  
 RT producing organism Amycolatopsis mediterranei DSM5908.  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR HSPB: CA76549.1; -;  
 DR HSPB: Q00441.1; 10X;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450; 1.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 406 AA; 44795 MW; 203C2AC5293A0F13 CRC64;

Query Match 36.8%; Score 7; DB 2; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPD 10  
 |||||  
 Db 394 AFVDCPD 400

## RESULT 14

OBRN03 PRELIMINARY; PRT; 406 AA.  
 ID OBRN03;  
 DT 01-JUN-2002 (TRENBLREL 21, Created)  
 DT 01-JUN-2002 (TRENBLREL 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL 21, Last annotation update)  
 DE OYXC.  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis.  
 RX NCBI\_TaxID:31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Zerbe K., Vrijsbloed J.W., Robinson J.A.;  
 RT "DNA sequence coding for P450 monooxygenases of vancomycin producer  
 RT Amycolatopsis orientalis."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF486630; AAL90879.1; -;  
 SQ SEQUENCE 406 AA; 45187 MW; 6C0E2EFA167A747A CRC64;

Query Match 36.8%; Score 7; DB 2; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPD 10  
 |||||  
 Db 394 AFVDCPD 400

## RESULT 15

O9VX29 PRELIMINARY; PRT; 653 AA.  
 ID O9VX29;  
 DT 01-MAY-2000 (TRENBLREL 13, Created)  
 DT 01-MAY-2000 (TRENBLREL 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL 21, Last annotation update)  
 DE CG12990 protein.  
 GN CG12990.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RX NCBI\_TaxID=7227;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Gelinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanalides P.G., Scher S.E., Li P.W., Hopkins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Miklos G.L.G.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,  
 RA April J.F., Aspray A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gehart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., McIntum K.A.,  
 RA Jellali M., Kalush F., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris D.M., Nelson D.L.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
 RA Palazzolo M., Pittman K.A., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,  
 RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 DR EMBL: AEO03506; AAF48752.1; -;  
 DR EMBL: AEO03506; AAF48752.1; -;  
 DR Flybase: FBgn030859; CG12990.  
 DR InterPro: IPR002656; Acyl\_transf\_3.  
 DR Pfam: PF01757; Acyl\_transf\_3; 1.  
 SQ SEQUENCE 653 AA; 74962 MW; 260525FDEA1B3856 CRC64;

Query Match 36.8%; Score 7; DB 5; Length 653;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SWALKAI 18  
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 Db 60 SWALKAI 66

Search completed: April 16, 2003, 16:36:39  
 Job time : 4.3087 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:18:40 : Search time 1.06076 seconds

(without alignments)  
527.016 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Perfect score: 106

Sequence: 1 TGTAFVDCPDSEWALKAE 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/prodata/1/aa/5A-COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/5B-COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6A-COMB.pep:\*  
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6: /cgn2\_6/prodata/1/aa/PCrus.COMB.pep:\*  
7: /cgn2\_6/prodata/1/aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	106	100.0	579 4 US-09-643-597-176	Sequence 176, App
2	106	100.0	579 4 US-09-643-597-176	Sequence 348, App
3	95	89.6	577 4 US-09-261-855-2	Sequence 2, Appli
4	48.5	45.8	309 3 US-09-109-205-1	Sequence 1, Appli
5	47	44.3	414 1 US-07-667-276A-4	Sequence 4, Appli
6	43	40.6	391 1 US-08-602-010A-6	Sequence 6, Appli
7	43	40.6	391 1 US-08-680-726A-6	Sequence 4, Appli
8	43	40.6	391 1 US-09-092-409-6	Sequence 6, Appli
9	42	39.6	885 4 US-09-342-648-9	Sequence 9, Appli
10	41.5	39.2	932 4 US-08-887-534A-45	Sequence 45, Appli
11	41	38.7	690 4 US-09-422-869-28	Sequence 28, Appli
12	41	38.7	759 1 US-08-676-967-1	Sequence 1, Appli
13	41	38.7	759 1 US-08-676-974-1	Sequence 1, Appli
14	41	38.7	759 2 US-09-098-487-1	Sequence 1, Appli
15	41	38.7	826 4 US-09-564-805-2	Sequence 224, App
16	41	38.7	826 4 US-09-564-805-224	Sequence 224, App
17	41	38.7	826 4 US-09-564-805-226	Sequence 80, Appli
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20	40.5	38.2	333 4 US-09-721-362-80	Sequence 228, App
21	40.5	38.2	837 4 US-09-564-805-228	Sequence 27, Appli
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23	40	37.7	80 1 US-07-881-075-10	Sequence 10, Appli
24	40	37.7	80 1 US-08-120-827-10	Sequence 10, Appli
25	40	37.7	80 1 US-08-478-675-10	Sequence 10, Appli
26	40	37.7	336 1 US-07-667-276A-8	Sequence 8, Appli
27	40	37.7	398 1 US-08-261-822A-16	Sequence 16, Appli

28	40	37.7	398 5 PCT-US95-07744A-16	Sequence 16, Appli
29	40	37.7	519 4 US-09-312-183A-3	Sequence 3, Appli
30	40	37.7	547 4 US-09-312-183A-2	Sequence 222, App
31	40	37.7	822 4 US-09-564-805-222	Sequence 71, Appli
32	39	36.8	267 4 US-08-818-112-71	Sequence 72, Appli
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34	39	36.8	267 4 US-09-056-556-71	Sequence 72, Appli
35	39	36.8	267 4 US-09-072-596-72	Sequence 3, Appli
36	39	36.8	381 2 US-08-858-052-3	Sequence 3, Appli
37	39	36.8	381 3 US-09-200-284-3	Sequence 1, Appli
38	39	36.8	906 1 US-08-094-889-1	Sequence 9, Appli
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44	38	35.8	57 4 US-09-435-242-33	Sequence 33, Appli
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## ALIGNMENTS

Result 1  
US-09-643-597-176  
Sequence 176, Application US/09643597  
Patent No. 6426072  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-176  
Query Match 100.0%; Score 106; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TGTAFVDCPDSEWALKAE 19  
DB 37 TGTAFVDCPDSEWALKAE 55  
RESULT 2  
US-09-643-597-348  
Sequence 348, Application US/09643597  
Patent No. 6426072  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.

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? APPLICANT: Wang, Aljun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? FILE REFERENCE: 210121.455C11
? CURRENT APPLICATION NUMBER: US/09/643,597
? NUMBER OF SEQ ID NOS: 2000-08-21
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 348
? LENGTH: 579
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-643-597-348

Query Match
Best Local Similarity 100.0%; Score 106; DB 4; Length 579;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDESMALKALE 19
DB 37 TGTAFTVDCPDESMALKALE 55

RESULT 3
US-09-261-855-2
? Sequence 2, Application US/09261855A
? Patent No. 6255055
? GENERAL INFORMATION:
? APPLICANT: Ross, Jeffrey
? TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
? FILE REFERENCE: 960296.95131
? CURRENT APPLICATION NUMBER: US/09/261,855A
? NUMBER OF SEQ ID NOS: 46
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 2
? LENGTH: 577
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-261-855-2

Query Match
Best Local Similarity 89.6%; Score 95; DB 4; Length 577;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDESMALKALE 19
DB 37 TGTAFTVDCPDESMALKALE 55

RESULT 4
US-09-109-205-1
? Sequence 1, Application US/09109205
? Patent No. 6057110
? GENERAL INFORMATION:
? APPLICANT: Lal, Preeti
? APPLICANT: Guegler, Karl J.
? APPLICANT: Gorgone, Gina
? APPLICANT: Corley, Neil C.
? APPLICANT: Baughn, Mariah R.
? APPLICANT: Yue, Henry
? TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,205
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0542 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT14
CLONE: 1511003

US-09-109-205-1

Query Match
Best Local Similarity 45.8%; Score 48.5; DB 3; Length 309;
Matches 11; Conservative 1; Mismatches 5; Indels 13; Gaps 1;

QY 1 TGTAFTVDCPDE-----SMALKA 17
DB 130 TCKKFLDCPDELMEKSPDVNFKAHMLWTYKA 159

RESULT 5
US-07-667-276A-4
? Sequence 4, Application US/07667276A
? Patent No. 5470971
? GENERAL INFORMATION:
? APPLICANT: Kondo, Keiji
? APPLICANT: Inouye, Masayori
? TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
? TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Welser & Associates
? STREET: 230 S. Fifteenth Street, Suite 500
? CITY: Philadelphia
? STATE: PA
? COUNTRY: USA
? ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,276A
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377,5351P
TELECOMMUNICATION INFORMATION:
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TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-667-276A-4

Query Match 44.3%; Score 47; DB 1; Length 414;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYAFVDCPDSEWALKAE 19  
DB 210 GYGVDFENKSYAEKATQ 227

RESULT 6  
US-08-602-010A-6  
Sequence 6, Application US/08602010A  
Patent No. 5753235

GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
ATTORNEY: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,010A  
FILING DATE: February 15, 1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223

INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-602-010A-6

Query Match 40.6%; Score 43; DB 1; Length 391;  
Best Local Similarity 42.1%; Pred. No. 47;  
Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 3 YAFVDC--PDSEWALKAE 19  
DB 153 YAVVSCWEPSPMKPECLE 171

RESULT 7  
US-08-680-726A-6  
Sequence 6, Application US/08680726A  
Patent No. 5604197

GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.  
ATTORNEY: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/680,726A  
FILING DATE: 12-JUL-1996

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46-C1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223

INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-680-726A-6

Query Match 40.6%; Score 43; DB 1; Length 391;  
Best Local Similarity 42.1%; Pred. No. 47;  
Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 3 YAFVDC--PDSEWALKAE 19  
DB 153 YAVVSCWEPSPMKPECLE 171

RESULT 8  
US-09-092-409-6  
Sequence 6, Application US/09092409  
Patent No. 6159478

GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
ATTORNEY: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,409  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/680,726  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:





TITLE OF INVENTION: Human Telomerase  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Science & Technology Law Group  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/676,967  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UCB96-055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415)343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-676-967-1  
Query Match 38.7%; Score 41; DB 1; Length 759;  
Best Local Similarity 47.1%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 2 GYAFVDCPDSEWALKAI 18  
DB 541 GYAFAEQEHKAL 557  
RESULT 13  
US-08-676-974-1  
Sequence 1, Application US/08676974  
Patent No. 5770422  
GENERAL INFORMATION:  
APPLICANT: COLLINS, KATHLEEN  
TITLE OF INVENTION: Human Telomerase  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Science & Technology Law Group  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/676,974  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UCB96-055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341

TELEFAX: (415)343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-676-974-1  
Query Match 38.7%; Score 41; DB 1; Length 759;  
Best Local Similarity 47.1%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 2 GYAFVDCPDSEWALKAI 18  
DB 541 GYAFAEQEHKAL 557  
RESULT 14  
US-09-098-487-1  
Sequence 1, Application US/09098487  
Patent No. 5917025  
GENERAL INFORMATION:  
APPLICANT: COLLINS, Kathleen  
TITLE OF INVENTION: Human Telomerase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Science & Technology Law Group  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/098,487  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UCB96-055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415)343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-09-098-487-1  
Query Match 38.7%; Score 41; DB 2; Length 759;  
Best Local Similarity 47.1%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 2 GYAFVDCPDSEWALKAI 18  
DB 541 GYAFAEQEHKAL 557  
RESULT 15  
US-09-564-805-2  
Sequence 2, Application US/09564805  
Patent No. 633403  
GENERAL INFORMATION:

Thu Apr 17 07:55:19 2003

us-09-897-778-176\_copy\_37\_55.ra

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; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 826
; TYPE: ERT
; ORGANISM: Homo sapiens
US-09-564-805-2

Query Match          38.7%; Score 41; DB 4; Length 826;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 GYAF--VDCPDSEW 13
   | | | | |
Db 303 GAFFVVECPDSEF 316

Search completed: April 16, 2003, 16:22:58
Job time : 3.06076 secs
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GenCore version 5.1.4\_P5-4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:21:35 ; Search time 1.43514 Seconds

(without alignments)  
1001.062 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55

Sequence: 1 TGYAFVDCPDSWALKAIE 19

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database: Published Applications-AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	579	10	US-09-735-705-176 Sequence 176, App
2	106	100.0	579	10	US-09-735-705-348 Sequence 348, App
3	106	100.0	579	10	US-09-850-716A-176 Sequence 176, App
4	106	100.0	579	10	US-09-850-716A-348 Sequence 348, App
5	106	100.0	579	10	US-09-897-778-176 Sequence 176, App
6	106	100.0	579	10	US-09-897-778-348 Sequence 348, App
7	106	100.0	579	10	US-09-897-778-446 Sequence 446, App
8	106	100.0	579	10	US-09-897-778-449 Sequence 449, App
9	106	100.0	586	10	US-09-850-716A-427 Sequence 427, App
10	106	100.0	586	10	US-09-897-778-427 Sequence 427, App
11	95	89.6	577	10	US-09-873-637-2 Sequence 2, Appli
12	93	87.7	18	10	US-09-897-778-465 Sequence 465, App
13	88	83.0	20	10	US-09-735-705-400 Sequence 400, App
14	88	83.0	20	10	US-09-850-716A-400 Sequence 400, App
15	88	83.0	20	10	US-09-897-778-400 Sequence 400, App
16	88	83.0	20	10	US-09-897-778-457 Sequence 457, App
17	80	75.5	20	10	US-09-735-705-399 Sequence 399, App
18	80	75.5	20	10	US-09-850-716A-399 Sequence 399, App
19	80	75.5	20	10	US-09-897-778-399 Sequence 399, App

20	80	75.5	620	10	US-09-764-864-1116 Sequence 1116, Ap
21	66	62.3	11	10	US-09-897-778-466 Sequence 466, App
22	48.5	45.8	303	9	US-09-925-299-851 Sequence 851, App
23	48.5	45.8	303	10	US-09-925-299-851 Sequence 851, App
24	44	41.5	359	9	US-10-025-367-25 Sequence 25, Appl
25	43	40.6	391	9	US-10-156-215-6 Sequence 6, Appli
26	43	40.6	578	10	US-09-925-300-1496 Sequence 1496, Ap
27	43	40.6	1179	10	US-09-821-883-29 Sequence 29, Appl
28	41.5	39.2	899	10	US-09-815-242-5356 Sequence 5356, App
29	41.5	39.2	932	10	US-09-815-242-12615 Sequence 12615, A
30	41	38.7	52	9	US-09-796-692-1087 Sequence 1087, Ap
31	41	38.7	52	9	US-09-796-692-1561 Sequence 1561, Ap
32	41	38.7	60	9	US-09-796-692-878 Sequence 878, App
33	41	38.7	68	9	US-09-796-692-887 Sequence 687, App
34	41	38.7	76	9	US-09-796-692-1076 Sequence 1076, Ap
35	41	38.7	82	9	US-09-796-692-1641 Sequence 1641, Ap
36	41	38.7	211	10	US-09-925-302-786 Sequence 786, App
37	41	38.7	521	10	US-09-925-300-1667 Sequence 1667, Ap
38	41	38.7	618	10	US-09-815-242-10864 Sequence 10864, A
39	41	38.7	690	10	US-09-768-877-28 Sequence 28, Appl
40	41	38.7	826	9	US-09-988-626-224 Sequence 224, App
41	41	38.7	826	9	US-09-988-626-224 Sequence 224, App
42	41	38.7	826	9	US-09-988-687-226 Sequence 226, App
43	41	38.7	826	9	US-09-988-687-224 Sequence 224, App
44	41	38.7	826	9	US-09-988-687-224 Sequence 224, App
45	41	38.7	826	9	US-09-988-687-226 Sequence 226, App

## ALIGNMENTS

RESULT 1  
US-09-735-705-176  
Sequence 176, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Litqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-176  
Query Match 100.0%; Score 106; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Ox 1 TGYAFVDCPDSWALKAIE 19  
Db 37 TGYAFVDCPDSWALKAIE 55  
RESULT 2  
US-09-735-705-348  
Sequence 348, Application US/09735705

```
Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Lijun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Jasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-735-705-348

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAFAVDCPDDESWALKATE 19
DB 37 TGAFAVDCPDDESWALKATE 55

RESULT 3
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-850-716A-176

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAFAVDCPDDESWALKATE 19
DB 37 TGAFAVDCPDDESWALKATE 55

RESULT 4
US-09-850-716A-348
: Sequence 348, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.

APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-897-778-176

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAFAVDCPDDESWALKATE 19
DB 37 TGAFAVDCPDDESWALKATE 55

RESULT 5
US-09-897-778-176
: Sequence 176, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Veddyck, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-897-778-176

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAFAVDCPDDESWALKATE 19
DB 37 TGAFAVDCPDDESWALKATE 55

RESULT 6
US-09-897-778-348
: Sequence 348, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Veddyck, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDDESMALKATE 19
DB 37 TGTAFTVDCPDDESMALKATE 55

RESULT 7
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDDESMALKATE 19
DB 37 TGTAFTVDCPDDESMALKATE 55

RESULT 8
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-449

Query Match          100.0%; Score 106; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDDESMALKATE 19
DB 37 TGTAFTVDCPDDESMALKATE 55

RESULT 9
US-09-850-716A-427
; Sequence 427, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: McNeill, Michael D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-427

Query Match          100.0%; Score 106; DB 10; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAFTVDCPDDESMALKATE 19
DB 44 TGTAFTVDCPDDESMALKATE 62

RESULT 10
US-09-897-778-427
; Sequence 427, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427
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LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-427

Query Match 100.0%; Score 106; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEMLKAIE 19  
|||||  
DB 44 TGYAFVDCPDSEMLKAIE 62

RESULT 11  
US-09-873-637-2  
Sequence 2, Application US/09873637  
Patent No. US20020061543A1  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/873.637  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-873-637-2

Query Match 89.6%; Score 95; DB 10; Length 577;  
Best Local Similarity 84.2%; Pred. No. 9.4e-07;  
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEMLKAIE 19  
|||||  
DB 37 SGYAFVDCPDSEMLKAIE 55

RESULT 12  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Mannerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darlick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897.778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 465  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-465

Query Match 87.7%; Score 93; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEMLK 16  
|||||  
DB 1 TGYAFVDCPDSEMLK 16

RESULT 13  
US-09-735-705-400  
Sequence 400, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735.705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-705-400

Query Match 83.0%; Score 88; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPDSEMLKAIE 19  
|||||  
DB 1 AFVDCPDSEMLKAIE 16

RESULT 14  
US-09-850-716A-400  
Sequence 400, Application US/09850716A  
Patent No. US20020115139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850.716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match 83.0%; Score 88; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AFVDCPDSEMLKAIE 19  
|||||  
DB 1 AFVDCPDSEMLKAIE 16

us-09-897-778-176\_copy\_37\_55.rabb

Page 5

	Query Match	83.0%	Score 88:	DB 10:	Length 20:
	Best Local Similarity	100.0%	Pred. No.	3.9e-07:	
	Matches	16:	Conservative	0:	Mismatches 0:
					Indels 0:
OY	4 AFVDCPD <del>S</del> MALKAT <del>E</del>	19			
Db	1 AFVDCPD <del>S</del> MALKAT <del>E</del>	16			

Search completed: April 16, 2003, 16:32:08  
Job time : 3.43514 secs







```
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESALKAE 19
   |||||
Db 5 TGYAFVDCPDESALKAE 23

RESULT 2
PCT-US01-47576-176
; Sequence 176, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Rafter, Neil
; APPLICANT: Rafter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-176

Query Match 100.0%; Score 106; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESALKAE 19
   |||||
Db 37 TGYAFVDCPDESALKAE 55

RESULT 3
PCT-US01-47576-348
; Sequence 348, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Rafter, Neil
; APPLICANT: Rafter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng

APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-348

Query Match 100.0%; Score 106; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESALKAE 19
   |||||
Db 37 TGYAFVDCPDESALKAE 55

RESULT 4
PCT-US01-47576-446
; Sequence 446, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Rafter, Neil
; APPLICANT: Rafter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-446

Query Match 100.0%; Score 106; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESALKAE 19
   |||||
Db 37 TGYAFVDCPDESALKAE 55

RESULT 5
PCT-US01-47576-449
; Sequence 449, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
```

```
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrik
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Beckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45503PC
CURRENT FILING DATE: 2001-11-30
CURRENT APPLICATION NUMBER: PCT/US01/47576
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 449
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-47576-449
```

```
Query Match          100.0%; Score 106; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 5,6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDSEWALKATE 19
    |||||
Db 37 TGYAFVDCPDSEWALKATE 55
```

```
RESULT 6
US-09-466-396A-176
; Sequence 176, Application US/09466396A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.45504
; CURRENT FILING DATE: 1999-12-17
; CURRENT APPLICATION NUMBER: US/09/466,396A
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-396A-176
```

```
Query Match          100.0%; Score 106; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 5,6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDSEWALKATE 19
    |||||
Db 37 TGYAFVDCPDSEWALKATE 55
```

```
RESULT 7
US-09-476-496A-176
; Sequence 176, Application US/09476496A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
```

```
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
FILE REFERENCE: 210121.45505
CURRENT APPLICATION NUMBER: US/09/476,496A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-476-496A-176
```

```
Query Match          100.0%; Score 106; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 5,6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDSEWALKATE 19
    |||||
Db 37 TGYAFVDCPDSEWALKATE 55
```

```
RESULT 8
US-09-480-884A-176
; Sequence 176, Application US/09480884A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45506
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-884A-176
```

```
Query Match          100.0%; Score 106; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 5,6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDSEWALKATE 19
    |||||
Db 37 TGYAFVDCPDSEWALKATE 55
```

```
RESULT 9
US-09-510-376A-176
; Sequence 176, Application US/09510376A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45507
; CURRENT APPLICATION NUMBER: US/09/510,376A
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-510-376A-176

Query Match 100.0%; Score 106; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESWALKATE 19  
DB 37 TGYAFVDCPDESWALKATE 55

RESULT 10  
US-09-542-615A-176  
Sequence 176, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542,615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-542-615A-176

Query Match 100.0%; Score 106; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESWALKATE 19  
DB 37 TGYAFVDCPDESWALKATE 55

RESULT 11  
US-09-542-615A-348  
Sequence 348, Application US/09542615A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542,615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-542-615A-348

Query Match 100.0%; Score 106; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESWALKATE 19  
DB 37 TGYAFVDCPDESWALKATE 55

RESULT 12  
US-09-606-421A-176  
Sequence 176, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-606-421A-176

Query Match 100.0%; Score 106; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESWALKATE 19  
DB 37 TGYAFVDCPDESWALKATE 55

RESULT 13  
US-09-606-421A-348  
Sequence 348, Application US/09606421A  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606,421A  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 354  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-606-421A-348

Query Match 100.0%; Score 106; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESWALKATE 19  
DB 37 TGYAFVDCPDESWALKATE 55

RESULT 14

US-09-606-421B-176

; Sequence 176, Application US/09606421B  
; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606,421B  
; CURRENT FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 176  
; LENGTH: 579

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-606-421B-176

Query Match

100.0%; Score 106; DB 20; Length 579;

Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKATE 19

DB 37 TGYAFVDCPDESMAKATE 55

RESULT 15

US-09-606-421B-348

; Sequence 348, Application US/09606421B  
; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606,421B  
; CURRENT FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 348  
; LENGTH: 579

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-606-421B-348

Query Match

100.0%; Score 106; DB 20; Length 579;

Best Local Similarity 100.0%; Pred. No. 5,6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDESMAKATE 19

DB 37 TGYAFVDCPDESMAKATE 55

Search completed: April 16, 2003, 16:29:54  
Job time : 14.7603 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:19:55 ; Search time 2.3399 Seconds  
(without alignments)  
1266.170 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_37\_55  
Perfect score: 106  
Sequence: 1 TGYAFVDCPDESWALKAE 19

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 705215 seqs, 155932251 residues

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents, AA, New:\*  
1: /cgn2\_6/p/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/p/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/p/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/p/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/p/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/p/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/p/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	43	US-10-313-986-482	Sequence 482, App
2	106	100.0	134	US-09-724-676-92917	Sequence 92917, A
3	106	100.0	134	US-09-724-676A-92917	Sequence 92917, A
4	106	100.0	492	US-09-724-676-92916	Sequence 92916, A
5	106	100.0	492	US-09-724-676A-92916	Sequence 92916, A
6	106	100.0	558	US-09-724-676-92918	Sequence 92918, A
7	106	100.0	558	US-09-724-676A-92918	Sequence 92918, A
8	106	100.0	579	US-10-313-986-176	Sequence 176, App
9	106	100.0	579	US-10-313-986-348	Sequence 348, App
10	106	100.0	579	US-10-313-986-446	Sequence 446, App
11	106	100.0	579	US-10-313-986-449	Sequence 449, App
12	106	100.0	579	US-10-313-986-480	Sequence 480, App
13	106	100.0	579	US-10-313-986-484	Sequence 484, App
14	106	100.0	579	US-10-313-986-485	Sequence 485, App
15	106	100.0	586	US-10-313-986-427	Sequence 427, App
16	106	100.0	586	US-10-313-986-427	Sequence 427, App
17	95	89.6	572	US-09-724-676-48617	Sequence 48617, A
18	95	89.6	572	US-09-724-676A-48617	Sequence 48617, A
19	95	89.6	572	US-09-724-676-48618	Sequence 48618, A
20	95	89.6	572	US-09-724-676A-48618	Sequence 48618, A
21	95	89.6	577	US-10-313-986-500	Sequence 500, App
22	95	89.6	598	US-09-724-676-48616	Sequence 48616, A
23	95	89.6	598	US-09-724-676A-48616	Sequence 48616, A
24	95	89.6	598	US-09-724-676A-48621	Sequence 48621, A
25	95	89.6	598	US-09-724-676A-48621	Sequence 48621, A
26	95	89.6	602	US-09-724-676A-48619	Sequence 48619, A

27	95	89.6	602	US-09-724-676-48620	Sequence 48620, A
28	95	89.6	602	US-09-724-676A-48619	Sequence 48619, A
29	95	89.6	602	US-09-724-676A-48620	Sequence 48620, A
30	93	87.7	18	US-10-313-986-465	Sequence 465, App
31	88	83.0	20	US-10-313-986-400	Sequence 400, App
32	88	83.0	20	US-10-313-986-457	Sequence 457, App
33	88	83.0	20	US-10-313-986-508	Sequence 508, App
34	80	75.5	20	US-10-313-986-399	Sequence 399, App
35	80	75.5	20	US-10-313-986-470	Sequence 470, App
36	80	75.5	20	US-10-313-986-507	Sequence 507, App
37	80	75.5	20	US-09-513-999C-7342	Sequence 7342, App
38	80	75.5	556	US-60-453-135-11528	Sequence 11528, A
39	80	75.5	556	US-60-453-050-11528	Sequence 11528, A
40	80	75.5	587	US-10-313-986-501	Sequence 501, App
41	80	75.5	599	US-60-453-135-11527	Sequence 11527, A
42	80	75.5	599	US-60-453-050-11527	Sequence 11527, A
43	69	65.1	255	US-60-452-680-15601	Sequence 15601, A
44	69	65.1	555	PCT-US02-31357-40	Sequence 40, Appl
45	69	65.1	555	US-10-262-445-40	Sequence 40, Appl

## ALIGNMENTS

RESULT 1  
US-10-313-986-482  
Sequence 482, Application US/10313986  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: McNeely, Andrea  
APPLICANT: Matanabe, Yoshinori  
APPLICANT: Reed, Steven G.  
APPLICANT: Wang, Tonglong  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C19  
CURRENT APPLICATION NUMBER: US/10/313,986  
NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 482  
LENGTH: 43  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-482

Query Match 100.0%; Score 106; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.3e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDESWALKAE 19  
Db 5 TGYAFVDCPDESWALKAE 23

RESULT 2  
US-09-724-676-92917  
Sequence 92917, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92917

Query Match 100.0%; Score 106; DB 5; Length 134;

Thu Apr 17 07:55:19 2003

us-09-897-778-176\_copy\_37\_55.rapn

Page 2

```
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAE 19
Db 37 TGYAFVDCPDSEWALKAE 55

RESULT 3
US-09-724-676A-92917
; Sequence 92917, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92917

Query Match 100.0%; Score 106; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAE 19
Db 37 TGYAFVDCPDSEWALKAE 55

RESULT 4
US-09-724-676-92916
; Sequence 92916, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92916

Query Match 100.0%; Score 106; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAE 19
Db 37 TGYAFVDCPDSEWALKAE 55

RESULT 5
US-09-724-676A-92916
; Sequence 92916, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92916

Query Match 100.0%; Score 106; DB 5; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAE 19
Db 37 TGYAFVDCPDSEWALKAE 55

RESULT 6
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match 100.0%; Score 106; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAE 19
Db 37 TGYAFVDCPDSEWALKAE 55

RESULT 7
US-09-724-676A-92918
; Sequence 92918, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92918

Query Match 100.0%; Score 106; DB 5; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGYAFVDCPDSEWALKAE 19
Db 37 TGYAFVDCPDSEWALKAE 55

RESULT 8
US-10-313-986-176
; Sequence 176, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
```



```
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176
```

```
Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55
```

```
RESULT 9
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348
```

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Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55
```

```
RESULT 10
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-313-986-446
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Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55
```

```
RESULT 11
; Sequence 449, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-449
```

```
Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55
```

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RESULT 12
; Sequence 480, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-480
```

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Query Match          100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TGYAFVDCPDDESMALKATE 19
DB 37 TGYAFVDCPDDESMALKATE 55
```

```

RESULT 13
US-10-313-986-484
; Sequence 484, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 579
; TYPE: PRT
; ORGANISM: primate
US-10-313-986-484

Query Match
Best Local Similarity 100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 14
US-10-348-119-255
; Sequence 255, Application US/10348119
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 NP
; CURRENT APPLICATION NUMBER: US/10/348,119
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-119-255

Query Match
Best Local Similarity 100.0%; Score 106; DB 6; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 37 TGYAFVDCPDSEWALKATE 55

RESULT 15
US-10-313-986-427
; Sequence 427, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-427

Query Match
Best Local Similarity 100.0%; Score 106; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGYAFVDCPDSEWALKATE 19
Db 44 TGYAFVDCPDSEWALKATE 62

Search completed: April 16, 2003, 16:31:15
Job time : 3.339 secs

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GenCore version 5.1.4.P5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:22:25 ; Search time 2.52874 Seconds  
(without alignments)  
579.640 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51  
Sequence: 1 FVDCPDESWAL 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	23	ABR75070
2	11	100.0	18	23	ABR75069
3	11	100.0	20	23	ABR75027
4	11	100.0	20	23	ABR75061
5	11	100.0	579	21	ABR11328
6	11	100.0	579	21	ABR11365
7	11	100.0	579	23	ABR74960
8	11	100.0	579	23	ABR74997
9	11	100.0	579	23	ABR75053
10	11	100.0	579	23	ABR75054

11	11	100.0	586	23	ABR75048	Human lung tumour
12	11	100.0	619	22	ABG21963	Novel human diagno
13	9	81.8	20	23	ABR75026	Human lung tumour
14	7	63.6	209	22	ABG21961	Novel human diagno
15	7	63.6	266	22	ABG12593	Novel human diagno
16	7	63.6	577	20	AAV30649	A murine c-myc cod
17	7	63.6	583	22	ABG12592	Novel human diagno
18	5	45.5	49	15	AAK49438	Murine HLA-DRAp
19	5	45.5	49	15	AAK49589	Sequence of HLA-DR
20	5	45.5	52	23	ABP02466	Human OREF protein
21	5	45.5	53	23	ABP01689	Human OREF protein
22	5	45.5	54	23	ABP33654	Human OREF267 prot
23	5	45.5	63	20	AAV41340	Human secreted pro
24	5	45.5	71	22	ABG31221	Peptide #3872 enco
25	5	45.5	71	22	ABG36428	Peptide #3934 enco
26	5	45.5	71	22	ABR21780	Protein #3779 enco
27	5	45.5	71	22	AAW57186	Human brain expres
28	5	45.5	71	22	AAW65991	Human bone marrow
29	5	45.5	71	22	AAW17405	Peptide #3839 enco
30	5	45.5	71	22	AAW29927	Peptide #3964 enco
31	5	45.5	71	22	AAW05090	Peptide #3772 enco
32	5	45.5	93	23	ABG39212	Human peptide enco
33	5	45.5	93	23	ABP06400	Human OREF protein
34	5	45.5	94	22	ABR87388	Human gene 47 enco
35	5	45.5	94	23	ABG65366	Human albumin fusi
36	5	45.5	109	22	AAU29896	Novel human secret
37	5	45.5	122	22	AAU42819	Protonibacterium
38	5	45.5	135	23	ABP03056	Human OREF protein
39	5	45.5	144	22	AAU58517	Protonibacterium
40	5	45.5	150	21	AAU56957	Human prostate can
41	5	45.5	150	23	AAE22108	Human 48921 quantin
42	5	45.5	155	21	AAE01801	Rice M10 homologue
43	5	45.5	174	21	ABR41067	Human OREF ORF831
44	5	45.5	174	23	ABP10782	Human OREF protein
45	5	45.5	196	23	ABG02217	Novel human diagno

#### ALIGNMENTS

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RESULT 1
ABR75070
ID ABR75070 standard; Peptide: 11 AA.
XX
AC ABR75070;
XX
DT 01-MAY-2002 (first entry)
XX
DE L523S antigenic epitope Seq ID NO:466.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW Immune response.
XX
OS Homo sapiens.
XX
PN WO200200174-A2.
XX
PD 03-JAN-2002.
XX
PE 28-JUN-2001; 2001WO-US21065.
XX
PF 28-JUN-2000; 2000US-0606421.
XX
PR 02-AUG-2000; 2000US-0630940.
XX
PR 21-AUG-2000; 2000US-0643597.
XX
PR 15-SEP-2000; 2000US-0662786.
XX
PR 09-OCT-2000; 2000US-0685696.
XX
PR 12-DEC-2000; 2000US-0735705.
XX
PR 07-MAY-2001; 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
McNeill PD, Fanger N, Retter MW, Manterakis M, Fanger GR;
```

FI Vedvick TS, Carter D, Watanabe Y, Peckham DW:  
 X1 WPI; 2002-090513/12.  
 DR N-PSDB; ABL49300.  
 XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
 XX lung cancer or stimulating an immune response -  
 XX  
 XX  
 PS Claim 2, Page 168; 374pp: English.  
 XX  
 CC The present invention describes human lung tumour proteins. Human lung  
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production. Compositions  
 CC comprising the lung tumour proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumour proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to  
 CC ABB75070 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XQ  
 Sequence 11 AA:

```

Qy      1 FVDCPESMAL 11
        | | | | | | | |
Db      1 FVDCPESMAL 11

Query Match 100.0%; Score 11; DB 23; length 11;
Best Local Similarity 100.0%; Pred. No. 5, 7e-07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
ABB75069
ID ABB75069 standard; Peptide: 18 AA.
vv

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XX	01-MAY-2002	(first entry)
DT		
XX		
DE	Human lung tumour L5235 epitope SEQ ID NO:465.	
XX		
KN	Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine.	
XX	Immune response.	

XX Homo sapiens.  
 XS  
 XX  
 XX W0200200174-A2.  
 XX FN  
 XX 03-JAN-2002.  
 XX XD

PE	28-JUN-2001	2001W0-USJ1065.
XX	28-JUN-2000	2000US-0606421.
PR	09-AUG-2000	2000US-0633597.
PR	21-AUG-2000	2000US-0643597.
PR	15-SEP-2000	2000US-0662786.
PR	09-OCT-2000	2000US-0665696.
PR	12-DEC-2000	2000US-0735705.
07-MAY-2001	2001US-0850716.	

PA (CORI-) CORIXA CORP.  
XX  
XX  
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos M, Henderson RA;  
PI McNeill PD, Fanger N, Reiter MW, Warnerakis M, Fanger GR;  
XX Vedrick TS, Carter D, Watanabe Y, Peckham DW;  
PI  
PI  
DR WPI; 2002-090513/12.  
XX  
XX  
PI Polynucleotides encoding lung tumor polypeptides, useful for treating  
PI lung cancer or stimulating an immune response -  
XX  
XX  
XX Claim 2; Page 168; 374pp; English.  
XX

The present invention describes human lung cancer proteins, human lung cancer proteins and polynucleotides having cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung cancer proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung cancer proteins are useful for treating lung cancer, or CC stimulating an immune response. ABL189S9 to ABL149300 and ABB1946 to ABB175070 represent sequences used in the exemplification of the present invention.

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Query Match 100.0%; Score 11; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 8, 6e-07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVDCPDESMA 11
    |||
Db 5 FVDCPDESMA 15

```

RESULT 3  
ABB75027  
ID ABB75027 standard; Peptide: 20 AA.  
yy

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XX      01-MAY-2002  (first entry)
DT
XX
DE      Human lung tumour L523S peptide SEQ ID NO:400
VE

```

KW	Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW	immune response.
XX	
OS	
XX	Homo sapiens.
XX	
PN	W0200200174-A2.
XX	

PD	03-JAN-2002.	2001WO-US21065.
XD		
PF	28-JUN-2001.	2001WO-US21065.
XX		
PR	28-JUN-2000.	2000US-0606421.
PR	28-AUG-2000.	2000US-0630940.
PR	21-AUG-2000.	2000US-0643597.
PR	15-SEP-2000.	2000US-0652785.
PR	09-OCT-2000.	2000US-0685956.
PR	12-DEC-2000.	2000US-0737505.
PR	07-MAY-2001.	2001US-0850716.
XX		

PA (CORI-) CORIXA CORP.  
XX  
XX  
PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA  
PI McNeill PD, Fanger N, Reltter MW, Manneakis M, Fanger GR  
XX Vedvick TS, Carter D, Matanabe Y, Peckham DW,  
XX  
DR WPI, 2002-090513/12.  
XX

PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
PS Claim 2: Page 348; 374pp; English.  
XX  
XX The present invention describes human lung tumor proteins. Human lung  
CC tumor proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumor proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumor proteins are useful for treating lung cancer or  
CC stimulating an immune response. AB148959 to AB149300 and AB174946 to  
CC AB175070 represent sequences used in the exemplification of the present  
CC invention.  
CX

SQ Sequence 20 AA;

Query Match 100.0%; Score 11; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
 |||||  
 Db 2 FVDCPDESMA 12

## RESULT 4

ABB75061  
 ID ABB75061 standard; Peptide; 20 AA.

AC ABB75061;

XX 01-MAY-2002 (first entry)

DE Human lung tumour L5235 epitope SEQ ID NO:457.

KM Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX Immune response.

OS Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skelky YAN, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;

PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

PT Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Claim 2; Page 167; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

CC ABB75070 represent sequences used in the exemplification of the present

CC invention.

XX Sequence 20 AA;

Query Match 100.0%; Score 11; DB 23; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.4e-07;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11

|||

Db 2 FVDCPDESMA 12

## RESULT 5

AAB11328  
 ID AAB11328 standard; Protein; 579 AA.

XX AAB11328;

XX 21-FEB-2001 (first entry)

DE Human lung cancer-associated protein L5235.

KM Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

XX vaccine; detection.

OS Homo sapiens.

XX WO200061612-A2.

XX 19-OCT-2000.

XX 03-APR-2000; 2000WO-US08896.

XX 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

DR N-PSDB; AAC65900.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor

PT protein is used for detecting and monitoring progression of lung cancer

PT in a patient -

XX Claim 3; Page 186-188; 261pp; English.

XX This invention describes a novel isolated polypeptide (1) which

CC comprising an immunogenic portion of a lung tumor protein or variant (P2)

CC which have cytostatic activity. The polypeptides and polynucleotides are

CC used in compositions and vaccines to inhibit the development of cancer,

CC especially lung cancer, in a patient. Methods described in the invention

CC can be used to monitor the progression of a cancer by carrying out the

CC detection at subsequent time points and comparing the results from the

CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient

CC are treated with P2, polynucleotides encoding P2 or antigen presenting

CC cells expressing P2 and then administered to the patient to inhibit

XX development of cancer.

SQ Sequence 579 AA;

Query Match 100.0%; Score 11; DB 21; Length 579;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11

|||

Db 41 FVDCPDESMA 51

RESULT 6

AAB11365

ID AAB11365 standard; Protein; 579 AA.

XX AAB11365;

XX 21-FEB-2001 (first entry)

DE Human lung cancer associated antigen L5235.

```

XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection.
XX Homo sapiens.
OS WO200061612-A2.
PN 19-OCT-2000.
PD 03-APR-2000; 2000WO-US08896.
PF 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-046396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX
XX (CORI-) CORIXA CORP.
PA Wang T, Fan L;
PI WPI: 2000-628399/60.
PI N-PSDB: AAC66035.
DR
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient.
XX Claim 3; Page 259-261; 261pp; English.
XX
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer. In a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from a patient
CC at different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
XX Sequence 579 AA:
SQ
Query Match 100.0%; Score 11; DB 21; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVDCPDESWAL 11
DB 41 FVDCPDESWAL 51
RESULT 7
ID ABB74960 standard; Protein; 579 AA.
XX
XX ABB74960;
AC
XX 01-MAY-2002 (first entry)
DT
XX Human lung tumour L5235 protein sequence SEQ ID NO:176.
DE
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX Homo sapiens.
OS WO200200174-A2.
PN 03-JAN-2002.
PD
XX

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PF 28-JUN-2001; 2001WO-US21065.
XX
XX 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
PA Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnierakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
DR WPI: 2002-090513/12.
DR N-PSDB: ABL49119.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response.
XX Example 2; Page 267-268; 374pp; English.
XX
XX The present invention describes human lung tumour proteins, human lung
CC tumor proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL4939 to ABL4900 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 579 AA:
SQ
Query Match 100.0%; Score 11; DB 23; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVDCPDESWAL 11
DB 41 FVDCPDESWAL 51
RESULT 8
ID ABB74997 standard; Protein; 579 AA.
XX
XX ABB74997;
AC
XX 01-MAY-2002 (first entry)
DT
XX Human lung tumour L5235 protein sequence SEQ ID NO:348.
DE
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX Homo sapiens.
OS WO200200174-A2.
PN 03-JAN-2002.
PD
XX 28-JUN-2001; 2001WO-US21065.
PF 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.

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XX (CORI-) CORIXA CORP.
PA
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Veelvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR WPI: 2002-090513/12.
DR N-PSDB: ABL49254.
XX
PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
PS Example 2; Page 330-332; 374pp; English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
SO Sequence 579 AA;
XX
Query Match 100.0%; Score 11; DB 23; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FVDCPDESMAI 11
DB 41 FVDCPDESMAI 51
XX
RESULT 9
ABR75053
ID ABR75053 standard; Protein; 579 AA.
XX
AC ABR75053;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human lung tumour L523S recombinant protein sequence SEQ ID NO:446.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX
OS Homo sapiens.
XX
PN W0200200174-A2.
XX
PD 03-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-US21065.
XX
PR 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Veelvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR WPI: 2002-090513/12.
DR N-PSDB: ABL49297.

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XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
PS Claim 2; Page 365-367; 374pp; English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
SO Sequence 579 AA;
XX
Query Match 100.0%; Score 11; DB 23; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FVDCPDESMAI 11
DB 41 FVDCPDESMAI 51
XX
RESULT 10
ABR75054
ID ABR75054 standard; Protein; 579 AA.
XX
AC ABR75054;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human lung tumour L523S recombinant protein sequence SEQ ID NO:449.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX
OS Homo sapiens.
XX
PN W0200200174-A2.
XX
PD 03-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-US21065.
XX
PR 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Veelvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR WPI: 2002-090513/12.
DR N-PSDB: ABL49299.
XX
PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
PS Claim 2; Page 368-369; 374pp; English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions

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Query Match	100.0%	Score 11:	DB 23:	Length 579:
Best Local Similarity	100.0%	Pred. No. 1.6e-05:		
Matches 11:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0
1 FVDCPDESML 11				
41 FVDCPDESML 51				
RESULT 11				
AB075048				
ID AB075048 standard; Protein: 586 AA.				
AC AB075048:				
DT 01-MAY-2002 (first entry)				
XX Human lung tumour L5235 recombinant protein sequence SEQ ID NO:427.				
DE Human lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;				
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;				
KW Immune response.				
XX Homo sapiens.				
OS WO200200174-A2.				
XX WO200200174-A2.				
PD 03-JAN-2002.				
XX 03-JAN-2002.				
XX 28-JUN-2001; 2001WO-US21065.				
PF 28-JUN-2001; 2001WO-US21065.				
XX 28-JUN-2001; 2000US-0606421.				
PR 02-AUG-2000; 2000US-0630940.				
PR 21-AUG-2000; 2000US-0643597.				
PR 15-SEP-2000; 2000US-0662786.				
PR 12-OCT-2000; 2000US-0685696.				
PR 12-DEC-2000; 2000US-0735705.				
PR 07-MAY-2001; 2001US-0850716.				
XX 07-MAY-2001; 2001US-0850716.				
XX (CORI-) CORIXA CORP.				
PA (CORI-) CORIXA CORP.				
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;				
PI McNeill PD, Fanger N, Reiter MW, Marengakis M, Fanger GR;				
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;				
XX WPI: 2002-090513/12.				
DR N-PSDB: ABL49283.				
XX Polynucleotides encoding lung tumor polypeptides, useful for treating				
PT lung cancer or stimulating an immune response.				
XX Claim 2; Page 354-355; 374pp; English.				
CC The present invention describes human lung tumour proteins. Human lung				
CC tumour proteins and polynucleotides have cytostatic and immunostimulant				
CC activities, and can be used in vaccine production. Compositions				
CC comprising the lung tumour proteins, polynucleotides, antibodies,				
CC fusion proteins, T cell populations, or antigen presenting cells that				
CC express the lung tumour proteins are useful for treating lung cancer or				
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to				
CC ABL75070 represent sequences used in the exemplification of the present				
CC invention.				
XX Sequence 579 AA;				

	Query Match	100.0%:	Score 11:	DB 23:	Length 566:
	Best Local Similarity	100.0%:	Pred. No. 1.7e-05:		
	Matches 11:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
OY	I FVQCPDESMAL 11                     48 FVQCPDESMAL 58				
	RESULT 12				
ABG21963	ABG21963 standard; Protein; 619 AA.				
AC	ABG21963:				
XX	18-FEB-2002 (first entry)				
XX	Novel human diagnostic protein #21954.				
DE	Human: chromosome mapping; gene mapping; gene therapy; forensic;				
KM	food supplement; medical imaging; diagnostic; genetic disorder.				
XX	Homo sapiens.				
OS	MO200175067-A2.				
PN	11-OCT-2001.				
PD	30-MAR-2001; 2001WO-US08631.				
PE	31-MAR-2000; 2000US-0540217.				
PR	23-AUG-2000; 2000US-0649167.				
XX	(HYSE-) HYSEQ INC.				
PA	Dermanac RT, Liu C, Tang YT;				
PI	WPI: 2001-639362/73.				
DR	N-PSDB: AASB6150.				
XX	New isolated polynucleotide and encoded polypeptides, useful in				
PT	diagnostics, forensics, gene mapping, identification of mutations				
PT	responsible for genetic disorders or other traits and to assess				
PT	biodiversity -				
XX	Claim 20: SEQ ID NO 52322; 103bp; English.				
XX	The invention relates to isolated polynucleotide (I) and				
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,				
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome				
CC	and gene mapping, and in recombinant production of (II). The				
CC	polynucleotides are also used in diagnostics as expressed sequence tags				
CC	for identifying expressed genes. (I) is useful in gene therapy techniques				
CC	to restore normal activity of (II) or to treat disease states involving				
CC	quantifying a polypeptide in tissue, as molecular weight markers and as				
CC	a food supplement. (II) and its binding partners are useful for treating				
CC	imaging of sites expressing (II). (I) and (II) are useful for treating				
CC	disorders involving aberrant protein expression or biological activity.				
CC	The polypeptide and polynucleotide sequences have applications in				
CC	diagnostics, forensics, gene mapping, identification of mutations in				
CC	responsible for genetic disorders or other traits to assess biodiversity				
CC	and to produce other types of data and products dependent on DNA and				
CC	amino acid sequences. ABG00010-ABG30377 represent novel human				
CC	diagnostic amino acid sequences of the invention.				
CC	Note: The sequence data for this patent did not appear in the printed				
CC	specification, but was obtained in electronic format directly from WIPO				
CC	at ftp://ipo.int/pub/published_pct_sequences.				
XX	Sequence 619 AA:				
XX	Query Match	100.0%:	Score 11:	DB 22:	Length 619:
XX	Best Local Similarity	100.0%:	Pred No. 1.7e-05:		



Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESMAL 11  
 |||||||  
 Db 77 FVDCPDSESMAL 87

RESULT 13  
 ABB75026  
 ID ABB75026 standard; Peptide: 20 AA.

AC ABB75026;

DT 01-MAY-2002 (first entry)

DE Human lung tumour L5235 peptide SEQ ID NO:399.

KM Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX immune response.

OS Homo sapiens.

PN WO200200174-A2.

PD 03-JAN-2002.

PF 28-JUN-2001; 2001WO-US21065.

PR 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Ranger N, Rector MW, Marneakis M, Ranger GR;

PI Veveick TS, Carter D, Matanabe Y, Peckham DW;

DR WPI: 2002-090513/12.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Claim 2; Page 348; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

CC ABB75070 represent sequences used in the exemplification of the present

XX invention.

XX Sequence 20 AA;

XX

XX

XX ABB21961;  
 AC 18-FEB-2002 (first entry)  
 DT Novel human diagnostic protein #21952.  
 DE Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US08631.

PE 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PA Drmanac RT, Liu C, Tang YF;

PI WPI: 2001-639362/73.

DR N-PSDB; AAS86148.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 20; SEQ ID NO 52320; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polynucleotide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABB00010-ABB30377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from Wipro

CC at ftp.wipro.int/pub/published\_pcl\_sequences.

XX Sequence 209 AA;

XX

XX

XX

XX

XX ABB21961;  
 AC 18-FEB-2002 (first entry)  
 DT Novel human diagnostic protein #21952.  
 DE Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US08631.

PE 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PA Drmanac RT, Liu C, Tang YF;

PI WPI: 2001-639362/73.

DR N-PSDB; AAS86148.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 20; SEQ ID NO 52320; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polynucleotide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABB00010-ABB30377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from Wipro

CC at ftp.wipro.int/pub/published\_pcl\_sequences.

XX Sequence 209 AA;

XX

XX

XX

XX

XX 18-FEB-2002 (first entry)  
DT  
XX Novel human diagnostic protein #12584.  
DE  
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
DA 30-MAR-2001; 2001MO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI: 2001-639362/73.  
DR N-PSDB; AAS76780.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
XX Claim 20; SEQ ID NO 42952; 103bp; English.  
PS  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against, detecting or  
CC identifying polypeptides in assays, as molecular weight, and detecting as  
CC a food supplement. (I) is also used in diagnostics as a useful for  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. Abg00010-Abg03037 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
SQ Sequence 266 AA:  
  
Query Match 63.6%; Score 7; DB 22; Length 266;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVDCPDE 7  
|||  
DB 21 FVDCPDE 27

Search completed: April 16, 2003, 16:34:38  
Job time: 4.52874 secs

GenCore version 5.1.4.P5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:32:15 ; Search time 0.776683 Seconds  
(without alignments)  
416.711 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Sequence: 1 FVDCPDESMA1 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PTUTUS.COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	579	4	US-09-643-597-176
2	11	100.0	579	4	US-09-643-597-348
3	7	63.6	577	4	US-09-261-855-2
4	5	45.5	294	4	US-08-973-334-2
5	5	45.5	294	4	US-09-563-869A-2
6	5	45.5	294	4	US-08-548-489-2
7	5	45.5	309	3	US-09-109-205-1
8	5	45.5	325	4	US-09-088-435-1
9	5	45.5	534	3	US-08-875-223-8
10	5	45.5	826	4	US-09-564-805-2
11	5	45.5	826	4	US-09-564-805-224
12	5	45.5	826	4	US-09-564-805-226
13	5	45.5	1059	4	US-09-134-513-2
14	5	45.5	1070	2	US-08-633-770A-2
15	5	45.5	1255	3	US-08-947-823-3
16	5	45.5	1257	3	US-08-947-823-5
17	5	45.5	1529	4	US-09-134-001C-3945
18	5	45.5	1956	4	US-08-843-417-2
19	5	45.5	1957	4	US-08-669-656A-2
20	5	45.5	1957	4	US-08-669-656A-8
21	5	45.5	2132	4	US-08-669-656A-6
22	4	36.4	4	2	US-08-478-386A-7
23	4	36.4	4	2	US-08-293-597-7
24	4	36.4	4	2	US-08-388-653-7
25	4	36.4	4	2	US-08-473-985-7
26	4	36.4	4	2	US-08-483-898-7
27	4	36.4	4	3	US-09-087-716-7

28	4	36.4	4	3	US-09-157-753-7	Sequence 7, Appl
29	4	36.4	4	3	US-09-157-230-7	Sequence 7, Appl
30	4	36.4	4	3	US-09-087-811-7	Sequence 7, Appl
31	4	36.4	4	3	US-09-156-855-7	Sequence 7, Appl
32	4	36.4	4	4	US-09-158-010-7	Sequence 7, Appl
33	4	36.4	4	4	US-09-087-647-7	Sequence 7, Appl
34	4	36.4	4	4	US-09-302-629-7	Sequence 7, Appl
35	4	36.4	4	6	PCT-US94-01321-59	Sequence 59, Appl
36	4	36.4	4	5	PCT-US94-01321-60	Sequence 60, Appl
37	4	36.4	4	10	US-08-726-464B-8	Sequence 8, Appl
38	4	36.4	4	10	US-08-726-464B-11	Sequence 11, Appl
39	4	36.4	4	10	US-08-849-480A-19	Sequence 19, Appl
40	4	36.4	4	11	US-09-183-217-9	Sequence 9, Appl
41	4	36.4	4	16	US-08-769-745-27	Sequence 27, Appl
42	4	36.4	4	17	US-08-179-481-69	Sequence 69, Appl
43	4	36.4	4	17	US-08-743-200-4	Sequence 4, Appl
44	4	36.4	4	6	525643-9	Patent No. 525643
45	4	36.4	4	19	US-08-789-333F-20	Sequence 20, Appl

## ALIGNMENTS

```

RESULT 1
US-09-643-597-176
: Sequence 176, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaltanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-643-597-176

Query Match      100.0%, Score 11, DB 4, Length 579;
Best local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY      1 FVDCPDESMA1 11
Db      41 FVDCPDESMA1 51

RESULT 2
US-09-643-597-348
: Sequence 348, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaltanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.

```

APPLICANT: Wang, Aijun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-348

Query Match 100.0%; Score 11; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPESMAL 11  
Db 41 FVDCPESMAL 51

RESULT 3  
US-09-261-855-2  
Sequence 2, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261,855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-2

Query Match 63.6%; Score 7; DB 4; Length 577;  
Best Local Similarity 100.0%; Pred. No. 0.84;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDE 7  
Db 41 FVDCPDE 47

RESULT 4  
US-08-973-334-2  
Sequence 2, Application US/08973334  
Patent No. 6261551  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Gao, Guang-Ping  
TITLE OF INVENTION: Recombinant Adenovirus and Adeno-  
TITLE OF INVENTION: Associated Virus, Cell Lines, and  
TITLE OF INVENTION: Methods of Production and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 No. 626151Irlstown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA

ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.0 Version 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,334  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/462,014  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/549,489  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNP/PNO12C1PUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-973-334-2

Query Match 45.5%; Score 5; DB 4; Length 294;  
Best Local Similarity 100.0%; Pred. No. .86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ESMAL 11  
Db 118 ESMAL 122

RESULT 5  
US-09-563-869A-2  
Sequence 2, Application US/09563869A  
Patent No. 6270996  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Gao, Guang-Ping  
TITLE OF INVENTION: Recombinant Adenovirus and Adeno-  
TITLE OF INVENTION: Associated Virus, Cell Lines, and  
TITLE OF INVENTION: Methods of Production and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 No. 6270996Irlstown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.0 Version 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/563,869A  
FILING DATE: 03-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/973,334  
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/549,489  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNP/NO12CIPUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-563-869A-2

Query Match 45.5%; Score 5; DB 4; Length 294;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESMAL 11  
DB 118 ESMAL 122

RESULT 6  
US-08-549-489-2  
Sequence 2, Application US/08549489  
Patent No. 6281010  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Gao, Guang-Ping  
TITLE OF INVENTION: No. 6281010e1 Adenovirus Gene Therapy Vehicle  
TITLE OF INVENTION: and Cell Line  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 No. 6281010Isttown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/549,489  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/462,014  
FILING DATE: 08-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNP/NO13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 294 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-549-489-2

Query Match 45.5%; Score 5; DB 4; Length 294;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ESMAL 11  
DB 118 ESMAL 122

RESULT 7  
US-09-109-205-1  
Sequence 1, Application US/09109205  
Patent No. 6057140  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Guegler, Karl J.  
APPLICANT: Gorgone, Gina  
APPLICANT: Corley, Neil C.  
APPLICANT: Baughn, Mariah R.  
APPLICANT: Yue, Henry  
TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,205  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cetrone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0542 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT14  
CLONE: 1511003  
US-09-109-205-1

Query Match 45.5%; Score 5; DB 3; Length 309;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DCPDE 7  
DB 136 DCPDE 140

RESULT 8  
US-09-088-435-1  
Sequence 1, Application US/09088435  
Patent No. 6277619

GENERAL INFORMATION:  
APPLICANT: LAL, PREETI  
APPLICANT: CORLEY, NEIL C.  
APPLICANT: GUEGLER, KARL J.  
APPLICANT: PATTERSON, CHANDRA  
TITLE OF INVENTION: SERINE DEHYDRATASE HOMOLOG  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Certone, Michael C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: FR-0512 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-853-0535  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: TPI1A2S08  
CLONE: 2752518  
US-09-088-435-1

Query Match 45.5%; Score 5; DB 4; Length 325;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESMAL 11  
DB 22 ESMAL 26

RESULT 9  
US-08-875-223-8  
Sequence 8, Application US/08875223  
Patent No. 6127175  
GENERAL INFORMATION:  
APPLICANT: VIGNE, Emmanuelle  
APPLICANT: PERRICAUDET, Michel  
APPLICANT: DEDIEU, Jean-Francois  
APPLICANT: ORSINI, Cecile  
APPLICANT: YEH, Patrice  
APPLICANT: LATTA, Marlene  
APPLICANT: PROST, Edouard  
TITLE OF INVENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT  
TITLE OF INVENTION: ADENOVIRUSES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcoia Road, Mailstop 3043  
CITY: Collegeville

STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,223  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/00747  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/06532  
FILING DATE: 01-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/10541  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR WO FR96/00088  
FILING DATE: 19-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehlner Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: ST95005G1-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-223-8

Query Match 45.5%; Score 5; DB 3; Length 534;  
Best Local Similarity 100.0%; Pred. No. 1,46+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESMAL 11  
DB 358 ESMAL 362

RESULT 10  
US-09-564-805-2  
Sequence 2, Application US/09564805  
Patent No. 633403  
GENERAL INFORMATION:  
APPLICANT: Tavligian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility  
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1999-11-05  
PRIOR APPLICATION NUMBER: 09/434,382  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 826  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-564-805-2

Query Match 45.5%; Score 5; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CPDES 8  
DB 311 CPDES 315

RESULT 11  
US-09-564-805-224  
Sequence 224, Application US/09564805  
Patent No. 6333403  
GENERAL INFORMATION:  
APPLICANT: Tavligian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Myriad Genetics, Inc.  
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
CURRENT FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: 09/434,382  
PRIOR FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 224  
LENGTH: 826  
TYPE: PRT  
ORGANISM: Pan troglodytes  
US-09-564-805-224

Query Match 45.5%; Score 5; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CPDES 8  
DB 311 CPDES 315

RESULT 12  
US-09-564-805-226  
Sequence 226, Application US/09564805  
Patent No. 6333403  
GENERAL INFORMATION:  
APPLICANT: Tavligian, Sean V.  
APPLICANT: Teng, David H.F.  
APPLICANT: Simard, Jacques  
APPLICANT: Rommens, Johanna M.  
APPLICANT: Myriad Genetics, Inc.  
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes  
FILE REFERENCE: 2318-258  
CURRENT APPLICATION NUMBER: US/09/564,805  
CURRENT FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/107,468  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: 09/434,382  
PRIOR FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 240  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 226  
LENGTH: 826  
TYPE: PRT  
ORGANISM: Gorilla gorilla

US-09-564-805-226

Query Match 45.5%; Score 5; DB 4; Length 826;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CPDES 8  
DB 311 CPDES 315

RESULT 13  
US-09-134-513-2  
Sequence 2, Application US/09134513  
Patent No. 6210964  
GENERAL INFORMATION:  
APPLICANT: Brown, Edward M.  
APPLICANT: Diaz, Ruben  
APPLICANT: Bai, Mei  
APPLICANT: Quinn, Stephen J.  
TITLE OF INVENTION: The Avian Extracellular Calcium Sensing  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Vison & Elkins L.L.P.  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.  
ZIP: 20004-1008  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,513  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanzo, Michael A.  
REGISTRATION NUMBER: 36,912  
REFERENCE/DOCKET NUMBER: BRI331/13003  
TELEPHONE: (202)639-6585  
TELEFAX: (202)639-6604  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1059 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
US-09-134-513-2

Query Match 45.5%; Score 5; DB 4; Length 1059;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
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QY 2 VDCPD 6  
DB 565 VDCPD 569

RESULT 14  
US-08-633-770A-2  
Sequence 2, Application US/08633770A  
Patent No. 5908760  
GENERAL INFORMATION:  
APPLICANT: Bojsen, Kirsten  
APPLICANT: Yu, Shukun  
APPLICANT: Kregh, Karsten

Thu Apr 17 07:55:19 2003

us-09-897-778-176\_copy\_41\_51.Oligo.ra1

Page 6

```

APPLICANT: Christensen, Tove
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYO06.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-633-770A-2

Query Match 45.5%; Score 5; DB 2; Length 1070;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ESWAL 11
DB 586 ESWAL 590

RESULT 15
US-08-947-823-3
Sequence 3, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isouhli
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-947-823-3

Query Match 45.5%; Score 5; DB 3; Length 1255;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PDESH 9
DB 679 PDESH 683
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Job time : 2.77668 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:36:47 ; Search time 1.26437 seconds  
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US-09-897-778-176\_COPY 41.51

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Sequence:      1 FVDCPDSESWAL 11
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Minimum DB seq length: 0

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- 2: /cgn2\_6/p/odata/1/pubpaa/FCIT\_NEM\_PUB\_pdp.\*
- 3: /cgn2\_6/p/odata/1/pubpaa/US06\_NEM\_PUB\_pdp.\*
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- 8: /cgn2\_6/p/odata/1/pubpaa/US08\_PUBCOMB\_pdp.\*
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- 10: /cgn2\_6/p/odata/1/pubpaa/US09\_PUBCOMB\_pdp.\*
- 11: /cgn2\_6/p/odata/1/pubpaa/US10\_NEM\_PUB\_pdp.\*
- 12: /cgn2\_6/p/odata/1/pubpaa/US10\_PUBCOMB\_pdp.\*
- 13: /cgn2\_6/p/odata/1/pubpaa/US60\_NEM\_PUB\_pdp.\*
- 14: /cgn2\_6/p/odata/1/pubpaa/US60\_PUBCOMB\_pdp.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	11	100.0	11	10	US-09-897-778-466	Sequence 466, App
2	11	100.0	18	10	US-09-897-778-465	Sequence 465, App
3	11	100.0	20	10	US-09-735-705-400	Sequence 400, App
4	11	100.0	20	10	US-09-850-716A-400	Sequence 400, App
5	11	100.0	20	10	US-09-897-778-400	Sequence 400, App
6	11	100.0	20	10	US-09-897-778-457	Sequence 457, App
7	11	100.0	579	10	US-09-735-705-176	Sequence 176, App
8	11	100.0	579	10	US-09-735-705-348	Sequence 348, App
9	11	100.0	579	10	US-09-850-716A-176	Sequence 176, App
10	11	100.0	579	10	US-09-850-716A-348	Sequence 348, App
11	11	100.0	579	10	US-09-897-778-176	Sequence 176, App
12	11	100.0	579	10	US-09-897-778-348	Sequence 348, App
13	11	100.0	579	10	US-09-897-778-446	Sequence 446, App
14	11	100.0	579	10	US-09-897-778-449	Sequence 449, App
15	11	100.0	586	10	US-09-850-716A-427	Sequence 427, App
16	11	100.0	586	10	US-09-897-778-427	Sequence 427, App
17	9	81.8	20	10	US-09-735-705-399	Sequence 399, App
18	9	81.8	20	10	US-09-850-716A-399	Sequence 399, App
19	9	81.8	20	10	US-09-897-778-399	Sequence 399, App

20	7	63.6	577	10	US-09-873-637-2	Sequence 2, Appl
21	5	45.5	91	10	US-09-864-761-37078	Sequence 37078, A
22	5	45.5	74	10	US-09-789-561-129	Sequence 129, App
23	5	45.5	119	9	US-10-007-270-26	Sequence 26, Appl
24	5	45.5	150	10	US-09-940-8364-9	Sequence 9, Appl
25	5	45.5	150	10	US-09-925-300-1535	Sequence 1535, Ap
26	5	45.5	235	10	US-09-803-28864-4	Sequence 4, Appl
27	5	45.5	294	9	US-10-155-649-2	Sequence 2, Appl
28	5	45.5	298	10	US-09-815-242-5142	Sequence 5142, Ap
29	5	45.5	303	9	US-09-925-259-851	Sequence 851, App
30	5	45.5	303	10	US-09-925-259-851	Sequence 851, App
31	5	45.5	357	10	US-10-260-871-128	Sequence 128, App
32	5	45.5	357	10	US-09-815-242-10981	Sequence 10981, A
33	5	45.5	432	9	US-10-007-270-19	Sequence 19, Appl
34	5	45.5	618	10	US-09-815-242-10864	Sequence 10864, A
35	5	45.5	761	9	US-09-147-947-4	Sequence 4, Appl
36	5	45.5	826	9	US-09-988-656-2	Sequence 2, Appl
37	5	45.5	826	9	US-09-988-656-224	Sequence 224, App
38	5	45.5	826	9	US-09-988-656-226	Sequence 226, App
39	5	45.5	826	9	US-09-988-657-2	Sequence 2, Appl
40	5	45.5	826	9	US-09-988-667-224	Sequence 224, App
41	5	45.5	826	9	US-09-988-667-226	Sequence 226, App
42	5	45.5	850	10	US-09-888-615-108	Sequence 108, App
43	5	45.5	1070	9	US-09-423-126-4	Sequence 4, Appl
44	5	45.5	1070	10	US-09-280-197-6	Sequence 6, Appl
45	5	45.5	1241	9	US-10-007-270-17	Sequence 17, Appl

## ALIGNMENTS

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RESULT 1
US-09-897-778-466
; Sequence 466, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 466
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-466

Query Match          100.0%; Score 11; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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Db       1 FVDCPDSEWAL 11

RESULT 2
US-09-897-778-465
; Sequence 465, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
APPLICANT: Wang, Tonglong

```

```

; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 FVDCPDSESWAL 15
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RESULT 3
; Sequence 400, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D. S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-400
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 FVDCPDSESWAL 12
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RESULT 4
US-09-850-716A-400
; Sequence 400, Application US/09850716A
; Patent No. US20020115139A1
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; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-400
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 FVDCPDSESWAL 12
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RESULT 5
US-09-897-778-400
; Sequence 400, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-400
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
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```

RESULT 6
US-09-897-778-457
; Sequence 457, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
```

```

; APPLICANT: Henderson, Robert A.
; APPLICANT: Beckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-457

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 2 FVDCPDSESMAL 12

RESULT 7
US-09-735-705-176
; Sequence 176, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-176

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 8
US-09-735-705-348
; Sequence 348, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
```

```

; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-348

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 9
US-09-850-716A-176
; Sequence 176, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 10
US-09-850-716A-348
; Sequence 348, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
```

```
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-348
```

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Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESVAL 11
        |||||
Db      41 FVDCPDESVAL 51
```

```
RESULT 11
US-09-897-778-176
Sequence 176, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Mamerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-176
```

```
Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESVAL 11
        |||||
Db      41 FVDCPDESVAL 51
```

```
RESULT 12
US-09-897-778-348
Sequence 348, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Mamerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
```

```
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 348
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-348
```

```
Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESVAL 11
        |||||
Db      41 FVDCPDESVAL 51
```

```
RESULT 13
US-09-897-778-446
Sequence 446, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Mamerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 446
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-446
```

```
Query Match          100.0%; Score 11; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESVAL 11
        |||||
Db      41 FVDCPDESVAL 51
```

```
RESULT 14
US-09-897-778-449
Sequence 449, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Mamerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 449  
LENGTH: 579  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-897-778-449

Query Match  
Best Local Similarity 100.0%; Score 11; DB 10; Length 579;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDESVAL 11  
|||||  
Db 41 FVDCPDESVAL 51

RESULT 15

US-09-850-716A-427  
Sequence 427, Application US/09850716A  
Patent NO. US20020115139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 427  
LENGTH: 586  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-850-716A-427

Query Match  
Best Local Similarity 100.0%; Score 11; DB 10; Length 586;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDESVAL 11  
|||||  
Db 48 FVDCPDESVAL 58

Search Completed: April 16, 2003, 16:48:44  
Job time : 2.26437 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:34:47 ; Search time 7.45977 Seconds  
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950.708 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 11

Sequence: 1 FVDCPESMAL 11

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Pending\_Patents\_AA\_Main:\*

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24: /cgn2\_6/ptodata/1/paa/US081.COMB.pep.\*  
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27: /cgn2\_6/ptodata/1/paa/US081.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	1 PCT-US01-47576-466	Sequence 466, App
2	11	100.0	11	22 US-09-897-778-466	Sequence 466, App
3	11	100.0	11	24 US-10-007-700-466	Sequence 466, App
4	11	100.0	11	25 US-10-117-982-466	Sequence 466, App
5	11	100.0	18	1 PCT-US01-47576-465	Sequence 465, App
6	11	100.0	18	22 US-09-897-778-465	Sequence 465, App

7	11	100.0	18	24	US-10-007-700-465	Sequence 465, App
8	11	100.0	18	25	US-10-117-982-465	Sequence 465, App
9	11	100.0	20	1	PCT-US01-47576-460	Sequence 460, App
10	11	100.0	20	1	PCT-US01-47576-457	Sequence 457, App
11	11	100.0	20	21	US-09-735-705-400	Sequence 400, App
12	11	100.0	20	22	US-09-850-716-400	Sequence 400, App
13	11	100.0	20	22	US-09-850-716-400	Sequence 400, App
14	11	100.0	20	22	US-09-897-778-460	Sequence 460, App
15	11	100.0	20	22	US-09-897-778-457	Sequence 457, App
16	11	100.0	20	24	US-10-007-700-460	Sequence 460, App
17	11	100.0	20	24	US-10-007-700-457	Sequence 457, App
18	11	100.0	20	25	US-10-117-982-400	Sequence 400, App
19	11	100.0	20	25	US-10-117-982-457	Sequence 457, App
20	11	100.0	43	25	US-10-117-982-482	Sequence 482, App
21	11	100.0	579	1	PCT-US01-47576-176	Sequence 176, App
22	11	100.0	579	1	PCT-US01-47576-348	Sequence 348, App
23	11	100.0	579	1	PCT-US01-47576-446	Sequence 446, App
24	11	100.0	579	1	PCT-US01-47576-448	Sequence 448, App
25	11	100.0	579	18	US-09-466-396A-176	Sequence 176, App
26	11	100.0	579	18	US-09-476-496A-176	Sequence 176, App
27	11	100.0	579	18	US-09-480-884A-176	Sequence 176, App
28	11	100.0	579	19	US-09-510-376A-176	Sequence 176, App
29	11	100.0	579	19	US-09-542-615A-176	Sequence 176, App
30	11	100.0	579	19	US-09-542-615A-348	Sequence 348, App
31	11	100.0	579	20	US-09-606-421A-176	Sequence 176, App
32	11	100.0	579	20	US-09-606-421A-348	Sequence 348, App
33	11	100.0	579	20	US-09-606-421B-176	Sequence 176, App
34	11	100.0	579	20	US-09-606-421B-348	Sequence 348, App
35	11	100.0	579	20	US-09-630-940A-176	Sequence 176, App
36	11	100.0	579	20	US-09-630-940A-348	Sequence 348, App
37	11	100.0	579	20	US-09-630-940B-176	Sequence 176, App
38	11	100.0	579	20	US-09-630-940B-348	Sequence 348, App
39	11	100.0	579	20	US-09-662-786-176	Sequence 176, App
40	11	100.0	579	20	US-09-662-786-348	Sequence 348, App
41	11	100.0	579	20	US-09-685-696-176	Sequence 176, App
42	11	100.0	579	20	US-09-685-696-348	Sequence 348, App
43	11	100.0	579	21	US-09-735-705-176	Sequence 176, App
44	11	100.0	579	21	US-09-735-705-348	Sequence 348, App
45	11	100.0	579	21	US-09-791-537-49019	Sequence 49019, A

## ALIGNMENTS

RESULT 1

PCT-US01-47576-466

Sequence 466, Application PC/TUS0147576

GENERAL INFORMATION:

APPLICANT: Corixa Corporation

APPLICANT: Wang, Tongfong

APPLICANT: Wang, Aijun

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Li, Samuel X.

APPLICANT: Kalos, Michael D.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

APPLICANT: Retter, Marc W.

APPLICANT: Durham, Margarita

APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Beckman, David W.

APPLICANT: Cai, Feng

APPLICANT: Foy, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455038C

CURRENT APPLICATION NUMBER: PCT/US01/47576

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US01-47576-466

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11  
DB 1 FVDCPDSESMAL 11

RESULT 2  
US-09-897-778-466  
Sequence 466, Application US/09897778  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnetakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darriek  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-466

Query Match 100.0%; Score 11; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11  
DB 1 FVDCPDSESMAL 11

RESULT 3  
US-10-007-700-466  
Sequence 466, Application US/10007700  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darriek  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Peckham, David W.  
APPLICANT: Cai, Feng  
APPLICANT: Foy, Teresa M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C17  
CURRENT APPLICATION NUMBER: US/10/007,700  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-007-700-466

Query Match 100.0%; Score 11; DB 24; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11  
DB 1 FVDCPDSESMAL 11

RESULT 4  
US-10-117-982-466  
Sequence 466, Application US/10117982  
GENERAL INFORMATION:  
APPLICANT: Foy, Teresa M.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darriek  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Mericle, Barbara  
APPLICANT: Spies, Gregory A.  
APPLICANT: Pan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C18  
CURRENT APPLICATION NUMBER: US/10/117,982  
CURRENT FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 484  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-117-982-466

Query Match 100.0%; Score 11; DB 25; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDSESMAL 11  
DB 1 FVDCPDSESMAL 11

RESULT 5  
PCT-US01-47576-465  
Sequence 465, Application PC/TUS0147576  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tonglong  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Fanger, Gary R.



```

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-465

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```

Query Match          100.0%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

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RESULT 6
US-09-897-778-465
; Sequence 465, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Matnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465

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Query Match          100.0%; Score 11; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 7
US-10-007-700-465
; Sequence 465, Application US/10007700
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.

```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Reller, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Cai, Feng
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-465

```

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Query Match          100.0%; Score 11; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 8
US-10-117-982-465
; Sequence 465, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-465

```

```

Query Match          100.0%; Score 11; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FVDCPDDESMAL 11
    |||
DB 5 FVDCPDDESMAL 15

```

```

RESULT 9
PCT-US01-47576-400
; Sequence 400, Application PC/TUS0147576

```

```

: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tongtong
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Melanabe, Yoshihiro
: APPLICANT: Beckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 400
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US01-47576-400

Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12

RESULT 10
PCT-US01-47576-457
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Wang, Tongtong
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Li, Samuel X.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: APPLICANT: Durham, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Melanabe, Yoshihiro
: APPLICANT: Beckman, David W.
: APPLICANT: Cal, Feng
: APPLICANT: Foy, Teresa M.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.45503PC
: CURRENT APPLICATION NUMBER: PCT/US01/47576
: CURRENT FILING DATE: 2001-11-30
: NUMBER OF SEQ ID NOS: 469
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT

: ORGANISM: Homo sapiens
PCT-US01-47576-457

Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12

RESULT 11
US-09-735-705-400
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 400
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-400

Query Match
Best Local Similarity 100.0%; Score 11; DB 21; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12

RESULT 12
US-09-850-716-400
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: TYPE: PRT
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SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716-400

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESWAL 11  
|||||  
DB 2 FVDCPDSESWAL 12

RESULT 13  
US-09-850-716A-400  
Sequence 400, Application US/09850716A  
GENERAL INFORMATION:  
APPLICANT: McNeill, Michael D.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESWAL 11  
|||||  
DB 2 FVDCPDSESWAL 12

RESULT 14  
US-09-897-778-400  
Sequence 400, Application US/09897778  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedrick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-400

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FVDCPDSESWAL 11  
|||||  
DB 2 FVDCPDSESWAL 12

RESULT 15  
US-09-897-778-457  
Sequence 457, Application US/09897778  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedrick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 457  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-457

Query Match  
Best Local Similarity 100.0%; Score 11; DB 22; Length 20;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESWAL 11  
|||||  
DB 2 FVDCPDSESWAL 12

Search completed: April 16, 2003, 16:45:13  
Job time : 8.45977 secs

2

3

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: April 16, 2003, 16:35:32 ; Search time 2.27586 Seconds

(without alignments)  
753,673 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 11

Sequence: 1 FVDCPDESWMAL 11

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched:

Word size: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database:

1: /cgn2.6/pdata1/paa/PCT\_NEW.COMB.pep:\*  
2: /cgn2.6/pdata1/paa/US06\_NEW.COMB.pep:\*  
3: /cgn2.6/pdata1/paa/US07\_NEW.COMB.pep:\*  
4: /cgn2.6/pdata1/paa/US08\_NEW.COMB.pep:\*  
5: /cgn2.6/pdata1/paa/US09\_NEW.COMB.pep:\*  
6: /cgn2.6/pdata1/paa/US10\_NEW.COMB.pep:\*  
7: /cgn2.6/pdata1/paa/US60\_NEW.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query length	DB ID	Description
1	11	100.0	11	US-10-313-986-466	Sequence 466, App
2	11	100.0	18	US-10-313-986-465	Sequence 465, App
3	11	100.0	20	US-10-313-986-457	Sequence 457, App
4	11	100.0	20	US-10-313-986-457	Sequence 457, App
5	11	100.0	20	US-10-313-986-457	Sequence 457, App
6	11	100.0	43	US-10-313-986-482	Sequence 482, App
7	11	100.0	134	US-09-724-676-92917	Sequence 92917, A
8	11	100.0	134	US-09-724-676-92917	Sequence 92917, A
9	11	100.0	432	US-09-724-676-92916	Sequence 92916, A
10	11	100.0	432	US-09-724-676-92916	Sequence 92916, A
11	11	100.0	358	US-09-724-676-92918	Sequence 92918, A
12	11	100.0	358	US-09-724-676-92918	Sequence 92918, A
13	11	100.0	358	US-10-313-986-176	Sequence 176, App
14	11	100.0	358	US-10-313-986-176	Sequence 176, App
15	11	100.0	358	US-10-313-986-176	Sequence 176, App
16	11	100.0	358	US-10-313-986-176	Sequence 176, App
17	11	100.0	358	US-10-313-986-176	Sequence 176, App
18	11	100.0	358	US-10-313-986-176	Sequence 176, App
19	11	100.0	358	US-10-313-986-176	Sequence 176, App
20	11	100.0	358	US-10-313-986-176	Sequence 176, App
21	11	100.0	358	US-10-313-986-176	Sequence 176, App
22	11	100.0	358	US-10-313-986-176	Sequence 176, App
23	11	100.0	358	US-10-313-986-176	Sequence 176, App
24	11	100.0	358	US-10-313-986-176	Sequence 176, App
25	11	100.0	358	US-10-313-986-176	Sequence 176, App
26	11	100.0	358	US-10-313-986-176	Sequence 176, App

27	7	63.6	572	5	US-09-724-676A-48617	Sequence 48617, A
28	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
29	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
30	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
31	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
32	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
33	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
34	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
35	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
36	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
37	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
38	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
39	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
40	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
41	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
42	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
43	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
44	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A
45	7	63.6	572	5	US-10-313-986-48618	Sequence 48618, A

## ALIGNMENTS

```

RESULT 1
US-10-313-986-466
Sequence 466, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C19
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 466
LENGTH: 11
ORIGIN: Homo sapiens
US-10-313-986-466
Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 1 FVDCPDESWMAL 11
Db 1 FVDCPDESWMAL 11
RESULT 2
US-10-313-986-465
Sequence 465, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C19
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 465
LENGTH: 18

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```

; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92917

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 134;
Pred. No. 1.3e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 8
US-09-724-676A-92917
; Sequence 92917, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92917
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92917

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 134;
Pred. No. 1.3e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 9
US-09-724-676-92916
; Sequence 92916, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92916

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 492;
Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 10
US-09-724-676A-92916
; Sequence 92916, Application US/09724676A
; GENERAL INFORMATION:

```

```

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92916
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92916

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 492;
Pred. No. 3.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 11
US-09-724-676-92918
; Sequence 92918, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-92918

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 558;
Pred. No. 4.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

RESULT 12
US-09-724-676A-92918
; Sequence 92918, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92918
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-92918

Query Match
Best Local Similarity 100.0%; Score 11; DB 5; Length 558;
Pred. No. 4.4e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESMAL 11
Db 41 FVDCPDDESMAL 51

```

```

RESULT 13
US-10-313-986-176
; Sequence 176, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

```

```

RESULT 14
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

```

```

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

```

```

RESULT 15
US-10-313-986-446
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

```

```

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-446

Query Match
Best Local Similarity 100.0%; Score 11; DB 6; Length 579;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51

```

```

Search completed: April 16, 2003, 16:47:26
Job time : 3.27586 secs

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GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:31:34 ; Search time 0.704434 Seconds  
(without alignments)  
1501.176 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 11

Sequence: 1 FVDCPDESMAL 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR.73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54.5	75	2	G97116	probable nucleic a
2	54.5	234	2	A12709	branched-chain ami
3	54.5	234	2	B97492	azlC family protei
4	54.5	310	2	T44857	probable hydroxyla
5	54.5	313	2	G84335	hypothetical prote
6	54.5	337	2	T30601	cytochrome P450 hy
7	54.5	460	2	G84246	phosphomannomutase
8	45.5	88	2	D87272	hypothetical prote
9	45.5	101	2	A82121	hypothetical prote
10	45.5	107	2	AG2581	phosphoribosyl-ATP
11	45.5	112	2	E97363	phosphoribosyl-ATP
12	45.5	118	2	T31213	hypothetical prote
13	45.5	133	2	S74640	hypothetical prote
14	45.5	136	2	T35632	probable transpos
15	45.5	140	2	B81146	AzC-related prote
16	45.5	160	2	C81877	hypothetical prote
17	45.5	164	2	T19795	hypothetical prote
18	45.5	182	2	B72689	hypothetical prote
19	45.5	190	2	E95420	hypothetical prote
20	45.5	196	2	T19794	hypothetical prote
21	45.5	198	2	E70357	conserved hypotet
22	45.5	214	2	AC2726	DNA-binding protei
23	45.5	217	2	A82491	frim protein VCA01
24	45.5	229	2	G97507	probable DNA-bind
25	45.5	230	2	JC5418	somatolactin precu
26	45.5	246	2	AD3574	branched-chain ami
27	45.5	261	1	S58496	ILAI protein - Ara
28	45.5	269	1	I55969	interleukin-1 beta
29	45.5	269	2	G96925	biotin-(acetyl-CoA

30	45.5	270	2	D72334	sugar kinase, pfkB
31	45.5	293	2	B64339	spermidine synthas
32	45.5	294	1	Q4ADC2	early E4 34k prote
33	45.5	294	2	A05071	pol polyprotein -
34	45.5	298	2	H83163	probable transcrip
35	45.5	307	2	T24832	hypothetical prote
36	45.5	324	2	B86819	oxidoreductase yj
37	45.5	328	1	S52352	glucose kinase - S
38	45.5	328	2	B89935	glucokinase (impor
39	45.5	347	2	F70851	probable parb prot
40	45.5	357	1	G64053	chorismate synthas
41	45.5	359	2	S27788	neutrophil oxidase
42	45.5	371	2	B69451	conserved hypotet
43	45.5	379	2	T41947	hypothetical prote
44	45.5	383	2	F90415	conserved hypotet
45	45.5	409	2	G90491	conserved hypotet

## ALIGNMENTS

## RESULT 1

G97116 probable nucleic acid binding protein, containing KH domain [Imported] - Clostridium

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 17-May-2002

C:Accession: G97116

R:Noelling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.  
J. Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: G97116

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-75 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK79722.1; PID:g15024725; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1756

C:Superfamily: Bacillus conserved hypothetical protein y1qc

Query Match 54.5% Score 6; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPDE 7  
DB 13 VDCPDE 18

## RESULT 2

A12709 branched-chain amino acid permease Atu1082 [Imported] - Agrobacterium tumefaciens (st

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Mar-2002

C:Accession: A12709

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: A12709

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAL42095.1; PID:g17739477; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu1082

A:Map position: circular chromosome  
C:Superfamily: hypothetical protein b2682

Query Match 54.5%; Score 6; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DESMAL 11  
DB 113 DESMAL 118

## RESULT 3

azIC family protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 01-Mar-2002

A:Accession: B97492  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Onorillo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Mairfeld, B.; Science 294, 2323-2328, 2001  
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A:Reference number: A97359; PMID:11743194

A:Accession: B97492  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-234 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK6891.1; PID:915156113; GSPDB:GN00169  
A:Gene: AGR\_C 2001  
A:Map position: circular chromosome  
C:Superfamily: hypothetical protein b2682

Query Match 54.5%; Score 6; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DESMAL 11  
DB 113 DESMAL 118

## RESULT 4

probable hydroxylase d [imported] - Amycolatopsis orientalis (fragment)  
C:Species: Amycolatopsis orientalis  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 16-Feb-2001

A:Accession: T44857  
R:Solenberg, P.J.; Matsushima, P.; Stack, D.R.; Wilkie, S.C.; Thompson, R.C.; Balcz, R.; submitted to the EMBL Data Library, January 1997  
A:Description: Production of hybrid glycopeptide antibiotics in vitro and in streptomycin  
A:Reference number: 222861  
A:Accession: T44857  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-310 <SOL>  
A:Cross-references: EMBL:U84350; PIDN:AAA9296.1  
A:Experimental source: strain C129.4  
C:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology F:146-282/Domain: cytochrome P450 homology <P45>

Query Match 54.5%; Score 6; DB 2; Length 310;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPD 6  
DB 299 FVDCPD 304

## RESULT 5

G84335  
hypothetical protein Vng1845c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

A:Accession: G84335  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; A>Title: Genome sequence of Halobacterium species NRC-1  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: G84335  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-313 <STO>  
A:Cross-references: GB:AE004437; NID:910581291; PIDN:ANG20051.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: VNG1845C

Query Match 54.5%; Score 6; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DESMAL 11  
DB 186 DESMAL 191

## RESULT 6

cytochrome P450 hydroxylase homolog PCZA361.27 - Amycolatopsis orientalis (fragment)  
N:Alternate names: PCZA361.27  
C:Species: Amycolatopsis orientalis  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 16-Feb-2001

A:Accession: T30601  
R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Leonard Chem. Biol. 3, 155-162, 1998  
A>Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin  
A:Reference number: 218804  
A:Accession: T30601  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-337 <VAN>  
A:Cross-references: EMBL:A1223998  
C:Superfamily: Bacillus cytochrome P450 homology <P45>  
F:173-309/Domain: cytochrome P450 homology <P45>

Query Match 54.5%; Score 6; DB 2; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPD 6  
DB 326 FVDCPD 331

## RESULT 7

phosphomannomutase [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

A:Accession: G84246  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leitbauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; A>Title: Genome sequence of Halobacterium species NRC-1  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: G84246  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-460 <STO>  
A:Cross-references: GB:AE004437; NID:910580465; PIDN:ANG19339.1; GSPDB:GN00138

C:Genetics:  
A:Gene: pmu2  
C:Superfamily: phosphonomonotase

Query Match 54.5%; Score 6; DB 2; Length 460;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPE 7  
DB 379 VDCPE 384

RESULT 8  
DB7272

hypothetical protein CC0189 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: DB7272

R:Nieman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Debay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolton, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: AB7249; MUID:21173698; PMID:11259647

A:Accession: DB7272

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-88 <STO>

A:Cross-references: GB:AE005673; MUID:913421310; PIDN:AAK22176.1; GSPDB:GN00148

C:Genetics:  
A:Gene: CC0189

Query Match 45.5%; Score 5; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCP 5  
DB 55 FVDCP 59

RESULT 9  
AH2121

hypothetical protein alr2527 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AH2121

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2121

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA874226.1; PID:917131619; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:  
A:Gene: alr2527

Query Match 45.5%; Score 5; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6  
DB 44 VDCPD 48

RESULT 10

AG2581

phosphoribosyl-ATP pyrophosphohydrolase hlsE [imported] - *Agrobacterium tumefaciens* (

C:Species: *Agrobacterium tumefaciens*

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002

C:Accession: AG2581

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woe, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl

Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG2581

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <KUR>

A:Cross-references: GB:AF008688; PIDN:AAU41069.1; PID:917738357; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: hlsE

A:Map position: circular chromosome

C:Superfamily: phosphoribosyl-ATP pyrophosphatase hlsE

Query Match 45.5%; Score 5; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PDESW 9  
DB 21 PDESW 25

RESULT 11  
E97363

phosphoribosyl-ATP pyrophosphatase (PRA-PH) [imported] - *Agrobacterium tumefaciens* (s

C:Species: *Agrobacterium tumefaciens*

C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002

C:Accession: E97363

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*

A:Reference number: A97359; PMID:11743194

A:Accession: E97363

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK85862.1; PID:915154901; GSPDB:GN00169

A:Gene: AGR\_C\_60

A:Map position: circular chromosome

C:Superfamily: phosphoribosyl-ATP pyrophosphatase hlsE

Query Match 45.5%; Score 5; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PDESW 9  
DB 26 PDESW 30

RESULT 12  
T31213

hypothetical protein 724 - *Sphingomonas aromaticivorans* plasmid pMW1

C:Species: *Sphingomonas aromaticivorans*

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T31213

R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.

submitted to the EMBL Data Library, July 1998

A:Description: Complete sequence of a 184 kb catabolic plasmid from *Sphingomonas arom*

A:Reference number: Z20992

A:Accession: T31213  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-118 <ROM>  
A:Cross-references: EMBL:AF079317; NID:93378261; PID:93378354; PIDN:AAD03937.1  
C:Genetics:  
A:Gene: plasmid pML1  
A:Note: orf724  
C:Superfamily: sphingomonas aromaticivorans plasmid pML1 hypothetical protein 724

Query Match 45.5%; Score 5; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 DCPDE 7  
DB 87 DCPDE 91

RESULT 13  
S74640  
hypothetical protein slr1780 - Synechocystis sp. (strain PCC 6803)  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S74640  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis S.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S74640  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-133 <KAN>  
A:Cross-references: EMBL:D90900; GB:AB001339; NID:91651768; PIDN:BA016792.1; PID:9165186  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: hypothetical protein slr1780

Query Match 45.5%; Score 5; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ESMAL 11  
DB 2 ESMAL 6

RESULT 14  
T35632  
probable transposase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 18-Aug-2000  
C:Accession: T35632  
R:Seeger, K.U.; Harris, D.; James, K.D.; Parhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999  
A:Reference number: 221584  
A:Accession: T35632  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-136 <SEE>  
A:Cross-references: EMBL:AL079356; PIDN:CAB45627.1; GSPDB:GN00070; SCOEDB:SC6G9.36C  
C:Genetics:  
A:Gene: SCOEDB:SC6G9.36C  
C:Superfamily: Streptomyces coelicolor probable transposase SC6G9.36C

Query Match 45.5%; Score 5; DB 2; Length 136;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DESMA 10  
DB 15 DESMA 19

RESULT 15  
B81146  
Zn1c-related protein NMB0892 [imported] - Neisseria meningitidis (strain MC58 serogro  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: B81146  
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Pizzi, M. Science 287, 1809-1815, 2000  
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Noxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: B81146  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140 <RET>  
A:Cross-references: GB:AE002441; GB:AE002098; NID:97226123; PIDN:AAFA1301.1; PID:9722 C:Genetics:  
A:Gene: NMB0892

Query Match 45.5%; Score 5; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 DESMA 10  
DB 94 DESMA 98

Search completed: April 16, 2003, 16:37:41  
Job time : 2.70443 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:23:10 ; Search time 0.559934 Seconds  
(without alignments)  
814.809 Million cell updates/sec

Title: us-09-897-778-176\_COPY\_41\_51

Perfect score: 11  
Sequence: 1 FVDCPDSESMAL 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	54.5	75	YH56_CLOAB	Q97196 clostridium
2	5	45.5	107	HIS2_AGR75	Q8UJ91 agrobacteri
3	5	45.5	133	Y54L_SYN3	P72777 synechocyst
4	5	45.5	174	ARR6_XENLA	P51645 xenopus lae
5	5	45.5	230	SOML_CARAU	P79697 carassius a
6	5	45.5	261	AXTA_ARATH	Q38828 arabidopsis
7	5	45.5	268	IL1B_RAT	Q63264 rattus norv
8	5	45.5	269	IL1B_MOUSE	P10749 mus musculu
9	5	45.5	293	SPEE_METJA	Q57761 methanococc
10	5	45.5	294	E434_ADE02	P03339 human adeno
11	5	45.5	294	POL_SMSAV	P03359 simian sarc
12	5	45.5	328	GLK_STRXY	O56198 staphylococ
13	5	45.5	357	AROC_HAEIN	P43675 haemophilus
14	5	45.5	379	DUT_HSV7J	P52341 human herpe
15	5	45.5	431	YAZI_SCHPO	Q10223 schizosacch
16	5	45.5	439	IFZG_ENCCU	O96719 encephalito
17	5	45.5	446	IFZG_SCHPO	O09130 schizosacch
18	5	45.5	471	IFZG_HUMAN	P41091 homo sapien
19	5	45.5	471	IFZG_MOUSE	O920n1 mus musculu
20	5	45.5	471	IF2H_MOUSE	O920h2 mus musculu
21	5	45.5	471	MANC_KLEPN	Q48462 klebsiella
22	5	45.5	471	MANC_SALMO	O01410 salmonella
23	5	45.5	471	RFM9_ECOLI	P37753 escherichia
24	5	45.5	473	FLIT_AGR75	O34171 agrobacteri
25	5	45.5	473	IFZG_DROME	O24208 dirosophila
26	5	45.5	493	YKAY_CAEEL	P34258 caenorinabdi
27	5	45.5	527	IFZG_YEAST	P32481 saccharomyc
28	5	45.5	545	SYK_STRCO	O9x895 streptomyce
29	5	45.5	677	SP87_DICDI	P54643 dictyosteli
30	5	45.5	761	NEFR_MOUSE	O08762 mus musculu
31	5	45.5	1165	POL_GALV	P21414 gibbon ape
32	5	45.5	1173	DPOL_RCMVM	O85428 rat cytoMeg
33	5	45.5	1377	RP0C_BORBU	O51349 borrelia bu

34	5	45.5	1419	1	LYS2_SCHPO	P40976 schizosacch
35	5	45.5	1471	1	MY54_YEAST	P32492 saccharomyc
36	5	45.5	1628	1	NAGH_CLOPE	P26831 clostridium
37	5	45.5	2359	1	COAH_RAT	O9e6D0 rattus norv
38	5	45.5	2365	1	COAH_MOUSE	O8e427 mus musculu
39	4	36.4	29	1	SCX2_LETIO	P80670 leturus qui
40	4	36.4	29	1	SCX3_LETIO	P80671 leturus qui
41	4	36.4	30	1	CRG2_SCOMA	P19865 scollodon w
42	4	36.4	36	1	PSBY_ODOSI	P49543 odontella s
43	4	36.4	58	1	FEI2_HSV2	P14345 herpes simp
44	4	36.4	65	1	TSYL_DENPO	P25518 dendroaspis
45	4	36.4	65	1	TXM2_NAJKA	P82463 naja naja k

## ALIGNMENTS

RESULT 1	YH56_CLOAB	STANDARD;	PRT;	75 AA.
AC	O97196:			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hypothetical protein CAC1756.			
GN	CAC1756.			
OS	Clostridium acetobutylicum.			
OC	Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
CC	Clostridium.			
OX	NCBI_TaxID=1488;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;			
RX	MEDLINE=21359325; PubMed=11466286;			
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,			
RA	Gidsov R., Lee H.W., Dubois J., Qiu D., Hitt J., Wolf Y.I.,			
RA	Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,			
RA	Bennett G.N., Koonin E.V., Smith D.R.;			
RT	"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";			
RT	J. Bacteriol. 183:4823-4838(2001).			
RL	J. Bacteriol. 183:4823-4838(2001).			
CC	-I- SIMILARITY: BELONGS TO THE UPF0109 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: AE007684; AAK79722.1;			
DR	PROSITE: PS50084; KH.TYPE.1; FALSE NEG.			
KW	Hypothetical protein, RNA-binding, Complete proteome.			
FT	DOMAIN			
FT	29			
FT	75			
FT	KH.			
SEQ	SEQUENCE 75 AA: 8170 MW; A68E2113FAAE2DE CRC64;			
Query Match	54.5%; Score 6; DB 1; Length 75;			
Best Local Similarity	100.0%; Pred. No. 0.53;			
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	2 VDCPDE 7			
OY				
DB	13 VDCPDE 18			
RESULT 2	HIS2_AGR75	STANDARD;	PRT;	107 AA.
AC	O80U91:			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			



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DR InterPro: IPR003575; Small_GTPase.
DR Pfam: PF00025; arf. 1.
DR SMART: SM00177; ARF. 1.
DR SMART: SM00010; small_GTPase. 1.
DR TIGRFAMs: TIGR00231; small_GTP. 1.
DR PROSITE: PS01019; ARF. 1.
DR GTP-binding: Multigene family; Myristate: Protein transport;
KM GTP-binding: Multigene family; Myristate: Protein transport;
KW GTP-binding: Multigene family; Myristate: Protein transport;
FT INIT_MER 0 0 BY SIMILARITY.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT NP_BIND 19 26 GTP (BY SIMILARITY).
FT NP_BIND 62 66 GTP (BY SIMILARITY).
FT NP_BIND 121 124 GTP (BY SIMILARITY).
SQ SEQUENCE 174 AA; 20056 MW; A6DA35CDADDF1A21 CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 1; Length 174;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6
DB 87 VDCPD 91

RESULT 5
SOML_CARAU STANDARD; PRT; 230 AA.
ID SOML_CARAU
AC P79697;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Somatolactin precursor (Sl).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97242175; PubMed-9125164;
RA Cheng K.W., Chan Y.H., Chen Y.D., Yu K.L., Chan K.M.;
RT "Sequence of a cDNA clone encoding a novel somatolactin in goldfish,
RT Carassius auratus."
RL Biochem. Biophys. Res. Commun. 232:282-287(1997).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATROPIN/PROLACTIN FAMILY.
CC -----
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CC -----
DR EMBL: U72940; AAC60098.1; -.
DR HSSP: P01246; IBST.
DR InterPro: IPR001230; Ptenyl_site.
DR InterPro: IPR001400; Somatolactin.
DR Pfam: PF00103; hormone. 1.
DR PROSITE: PS00266; SOMATOTROPIN_1; FALSE_NEG.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
DR Hormone: Glycoprotein; signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 230 SOMATOLACTIN.
FT DISULFID 28 38 BY SIMILARITY.
FT DISULFID 87 202 BY SIMILARITY.
FT DISULFID 219 227 BY SIMILARITY.
FT CARBOHYD 226 226 BY SIMILARITY.
SQ SEQUENCE 230 AA; 25735 MW; CBC5DB3476116DC CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 1; Length 230;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDCPD 6
DB 26 VDCPD 30

RESULT 6
AXIA_ARATH STANDARD; PRT; 261 AA.
ID AXIA_ARATH
AC Q38828;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Auxin-responsive protein IAA10 (Indoleacetic acid-induced protein 10).
GN IAA10 OR ATIG04100 OR F20D22.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE-95387393; PubMed-7658471;
RA Abel S., Nguyen M.D., Theologis A.;
RT "The PS-IAA4/5-like family of early auxin-inducible mRNAs in
RT Arabidopsis thaliana."
RL J. Mol. Biol. 251:533-549(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE-21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.D., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.D., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Landin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Juros J.S., Maiti R., Marzilli A.,
RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Taiton L.J., Tambunga G., Tortum M.J., Town C.D.,
RA Ullrich T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Ban J., Etgu P., Lee J.M.,
RA Tortum M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F20D22.13 (GI:3142299).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR
CC MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR CELL
CC GROWTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- INDUCTION: BY AUXIN.
CC -1- SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
CC -----
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CC -----

DR EMBL: U18412; AAC49051.1; -

DR EMBL: AC002411; AAC16750.1; -

DR EMBL: AF333396; AAC48760.1; -

DR InterPro: IPR003311; AUX\_1AA.

DR Pfam: PF02309; AUX\_1AA; 1.

KW Multigene family; Nuclear protein; Translation regulation.

FT DOMAIN 60

FT SEQUENCE 261 AA; 27878 MW; DE99194344815A14 CRC64;

SO

Query Match 45.5%; Score 5; DB 1; Length 261;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CPDES 8

DB 35 CPDES 39

RESULT 7

IL1B-RAT STANDARD; PRT; 268 AA.

AC 063264;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Interleukin-1 beta precursor (IL-1 beta).

GN IL1B.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Macrophage;

RA Feiser W., Freimark B.D.;

RL Submitted (Aug-1992) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL

CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE

CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -1- MISCELLANEOUS: THESE PROTEINS SERVE AS YET UNDEFINED FUNCTION.

CC PRECURSOR SEQUENCE BY A SPECIFIC HYDROPHOBIC SEGMENT IN THE

CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER

CC SECRETORY PROTEINS

CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY

CC -----

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CC -----

DR EMBL: M98820; AAA41426.1; -

DR HSSP: P10749; 2M1B.

DR InterPro: IPR002348; ILL\_HGF.

DR InterPro: IPR003502; ILL\_proprep.

DR InterPro: IPR000975; Interleukin\_1.

DR Pfam: PF00340; ILL\_1.

DR Pfam: PF02394; ILL\_proprep; 1.

DR PRINTS: PR00262; ILLHGF.

DR ProDom: PD002536; Interleukin\_1; 1.

DR SMART: SM00125; ILL\_1.

DR PROSITE: PS00253; INTERLEUKIN\_1; 1.

KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.

FT PROPEP 116

FT CHAIN 117

SO SEQUENCE 268 AA; 30644 MW; 109C19B8F92C42D CRC64;

Query Match 45.5%; Score 5; DB 1; Length 268;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CPDES 8

DB 42 CPDES 46

RESULT 8

IL1B-MOUSE STANDARD; PRT; 269 AA.

AC P10749;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Interleukin-1 beta precursor (IL-1 beta).

GN IL1B.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=87058957; Pubmed=3491144;

RA Gray P.W., Glaister D., Chen E., Goeddel D.V., Pennica D.;

RT "Two interleukin 1 genes in the mouse: cloning and expression of the

RT cDNA for murine Interleukin 1 beta."

RL J. Immunol. 137:3644-3648(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC MEDLINE=87117546; Pubmed=3492706;

RA Telford J.L., Macchia G., Masson A., Carinci V., Palla E., Meili M.;

RT "The murine interleukin 1 beta gene: structure and evolution."

RL Nucleic Acids Res. 14:9955-9963(1986).

RN [3]

RP SEQUENCE OF 118-139.

RC MEDLINE=88229074; Pubmed=2967326;

RA Huang J.J., Newton R.C., Rutledge S.J., Horuk R., Mathew J.B.,

RA Coughlin M., Lin Y.;

RT "Characterization of murine IL-1 beta. Isolation, expression, and

RT purification."

RL J. Immunol. 140:3838-3843(1988).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC MEDLINE=92222792; Pubmed=1807351;

RA van Oostum J., Priesle J.P., Grutter M.G., Schmitz A.;

RA "The structure of murine interleukin 1 beta at 2.8-A resolution."

RL J. Biol. Chem. 267:10519-10523(1992).

CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL

CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE

CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE

CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER

CC SECRETORY PROTEINS

CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY

CC -----

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RP SEQUENCE FROM N.A. / DSM 2661 / ATCC 43067;
RX STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
AC MEDLINE=96337999; PubMed=868887;
RA BULT C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake O., Olsen G.J., Fritchard L.M., Clayton R.A., Gocayne J.D.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Ueberback T.R., Kelley J.M., Peterson J.D., Sadov P.W., Hanna M.C.,
RA Cotton M.P., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:11058-1073(1996).
CC -1- CATALYTIC ACTIVITY: S-adenosylmethioninamine + putrescine = 5'-
CC methylthioadenosine + spermidine.
CC -1- PATHWAY: FIFTH (LAST) STEP IN THE BIOSYNTHESIS OF SPERMIDINE FROM
CC ARGININE AND METHIONINE.
CC -1- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
CC -----
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CC -----
DR EMBL: U67486; AAB98300.1; -
DR TIGR: MU0313; -
DR InterPro: IPR000051; SAM_bind.
DR InterPro: IPR001045; Spmiline_synthase.
DR Pfam: PF01564; Spermine_synth. 1.
DR TIGRFAMs: TIGR00417; sps1. 1.
DR PROSITE: PS01330; SPERMIDINE_SYNTHASE; 1.
KW Spermidine biosynthesis; Transferase; Complete proteome.
FT DOMAIN 85
FT BINDING TO DECARBOXYLATED SAM
FT (POPEPTAL).
SQ SEQUENCE 293 AA; 33899 MW; 8884A8C919E5457A CRC64;
Query Match 45.5%; Score 5; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 VDCPD 6
OY 11111
DB 162 VDCPD 166

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CC -----  
DR EMBL: J01917; NOT\_ANNOTATED\_CDS.  
DR PIR: A03805; Q4ADC2.  
KW Early protein.  
SQ SEQUENCE 294 AA; 34116 MW; F60C83A38240BE0C CRC64;

Query Match 45.5%; Score 5; DB 1; Length 294;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ESWAL 11  
Db 118 ESWAL 122

RESULT 11  
POL\_SMSAV STANDARD; PRT; 294 AA.  
AC P03359;  
DT 21-JUL-1986 (rel. 01, Created)  
DT 21-JUL-1986 (rel. 01, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE POL polyprotein (contains: Reverse transcriptase (EC 2.7.7.49))  
DE (fragment).  
GN POL.  
OS Simian sarcoma virus.  
OC Viruses; Retroviridae; Gammaretrovirus.  
OX NCBI\_TaxID=11817;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83144004; PubMed=6298772;  
RT Nucleotide sequence of the simian sarcoma virus genome:  
RT demonstration that its acquired cellular sequences encode the  
RT transforming gene product p28s1s.  
RL Proc. Natl. Acad. Sci. U.S.A. 80:731-735(1983).  
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate  
CC + (DNA)(N).  
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: V01201; CA24515.1; .  
DR PIR: A05071; A05071.  
DR InterPro: IPR001584; Rye.  
KW Pflam: PF00665; rye; 1.  
DR Transferase: RNA-directed DNA polymerase; Polypotein.  
FT NON\_TER 1  
SQ SEQUENCE 294 AA; 32719 MW; EE062CEFF9485717F CRC64;

Query Match 45.5%; Score 5; DB 1; Length 294;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PDESW 9  
Db 268 PDESW 272

RESULT 12  
GLK\_STAXY STANDARD; PRT; 328 AA.  
ID GLK\_STAXY

AC O56198;  
DT 15-JUL-1998 (rel. 36, Created)  
DT 15-JUL-1998 (rel. 36, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE Glucokinase (EC 2.7.1.2) (glucose kinase).  
DE GLKA.  
OS Staphylococcus xylosum.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1288;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=DSM 20267 / Isolate CZA;  
RX MEDLINE=96042090; PubMed=7592379;  
RA Wagner E., Marcandier S., Egster O., Deutscher J., Goetz F.,  
RA Brueckner R.;  
RT "Glucose kinase-dependent catabolite repression in Staphylococcus  
RT xylosum".  
RT J. Bacteriol. 177:6144-6152(1995).  
CC -1- CATALYTIC ACTIVITY: ATP + D-glucose - ADP + D-glucose 6-phosphate.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE ROK (NAGC/XLR) FAMILY.

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CC -----  
DR EMBL: X84332; CA459069.1; .  
DR InterPro: IPR000600; ROK\_family.  
DR InterPro: IPR004654; ROK\_glcA\_fam.  
DR Pflam: PF00480; ROK; 1.  
DR TIGRFAMs: TIGR00744; ROK\_glcA\_fam; 1.  
DR PROSITE: PS01125; ROK; 1.  
KW Transferase: kinase; Glycolysis; ATP-binding.  
SQ SEQUENCE 328 AA; 35032 MW; 9BF62206FA1B5DF CRC64;

Query Match 45.5%; Score 5; DB 1; Length 328;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCP 5  
Db 105 FVDCP 109

RESULT 13  
AROC\_HAEIN STANDARD; PRT; 357 AA.  
AC P43875;  
DT 01-NOV-1995 (rel. 32, Created)  
DT 01-NOV-1995 (rel. 32, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE Chorismate synthase (EC 4.6.1.4) (5-enolpyruvylshikimate-3-phosphate  
DE phosphatase).  
GN AROC OR H10196.  
OC Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Rd / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7342800;  
RA Felschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

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RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.:
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512(1995).
CC -1- CATALYTIC ACTIVITY: 5-O-(1-carboxyvinyl)-3-phosphoshikimate =
CC chorismate + phosphate.
CC -1- COFACTOR: REDUCED FLAVIN (BY SIMILARITY).
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC seventh step.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
CC
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CC
CC
CC EMBL: U32704; AAC21865.1; -
CC TIGR: H10196; -
CC InterPro: IPR000453; Chorismate_synth.
CC Pfam: PF01264; Chorismate_synth.1.
CC Prodom: PD002941; Chorismate_synth.1.
CC Tricore: TRIGR00033; aroc.1.
CC
CC PROSITE: PS00787; CHORISMATE_SYNTHASE_1; 1.
CC PROSITE: PS00788; CHORISMATE_SYNTHASE_2; 1.
CC PROSITE: PS00789; CHORISMATE_SYNTHASE_3; 1.
CC KEGG: Aromatic amino acid biosynthesis; Complete proteome.
SQ SEQUENCE 357 AA; 38691 MW; 4504562BADF68164 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CPDES 8
Db 185 CPDES 189

RESULT 14
DUT_HSV7J STANDARD; PRT; 379 AA.
ID DUT_HSV7J
AC P52341;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
DE (dUTPase) (dUTP pyrophosphatase).
GN U45.
OS Human herpesvirus (type 7 / strain J1) (HHV7).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
ON NCBI_TaxID=57278;
RX [1]
RP SEQUENCE FROM N.A.
RA Nicholas J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT
CC PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES
CC AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
CC URACIL CANNOT BE INCORPORATED INTO DNA.
CC -1- CATALYTIC ACTIVITY: dUTP + H(2)O -> dUMP + diphosphate.
CC -1- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
CC
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CC
CC EMBL: UA3400; AAC54707.1; -
CC InterPro: IPR001428; DeoxyUTPase.
CC Pfam: PF00692; dUTPase; 1.
CC KEGG: Hydrolyase; Nucleotide metabolism.
SQ SEQUENCE 379 AA; 43876 MW; 56C61E097B67AD7C CRC64;

Query Match 45.5%; Score 5; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DCPDE 7
Db 287 DCPDE 291

RESULT 15
YAZ1_SCHPO STANDARD; PRT; 431 AA.
ID YAZ1_SCHPO
AC Q10223;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C13D6.01 in chromosome I.
GN SPAC13D6.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxID=4896;
RX [1]
RP SEQUENCE FROM N.A.
RA SPRAIN-972;
RA MEDLINE=21648401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Slimmons M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
RA Welteens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs W., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt K., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen O., Potashkin J.,
RA Snpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
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CC
CC EMBL: Z69725; CAA93541.1; -
CC Hypothetical protein.
KW SEQUENCE 431 AA; 49623 MW; 132FB0919646AC9F CRC64;

```

Query Match 45.5%; Score 5; DB 1; Length 431;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 DCPDE 7  
11111  
DB 171 DCPDE 175  
Search completed: April 16, 2003, 16:35:28  
Job time : 4.55993 Secs

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# OM protein - protein search, using sw model

Run on: April 16, 2003, 16:18:40 ; Search time 0.614121 Seconds  
(without alignments)  
527.016 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66

Sequence: 1 FVDCPDESMAL 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued Patents, AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCFUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	579	4 US-09-643-597-176	Sequence 176, App
2	66	100.0	579	4 US-09-643-597-348	Sequence 348, App
3	59	89.4	577	4 US-09-261-855-2	Sequence 2, Appli
4	40	60.6	309	3 US-09-109-205-1	Sequence 16, Appli
5	38	57.6	398	1 US-08-261-822A-16	Sequence 16, Appli
6	38	57.6	398	5 PCT-US95-07744A-16	Sequence 2, Appli
7	38	57.6	826	4 US-09-564-805-2	Sequence 16, Appli
8	38	57.6	826	4 US-09-564-805-224	Sequence 224, App
9	38	57.6	826	4 US-09-564-805-226	Sequence 226, App
10	37	56.1	430	4 US-09-149-476-707	Sequence 707, App
11	37	56.1	822	4 US-09-564-805-222	Sequence 222, App
12	37	56.1	885	4 US-09-342-648-9	Sequence 9, Appli
13	37	56.1	1044	2 US-08-777-405A-2	Sequence 2, Appli
14	37	56.1	1044	2 US-08-977-871A-2	Sequence 2, Appli
15	37	56.1	1044	2 US-09-225-951-2	Sequence 2, Appli
16	36	54.5	120	1 US-08-542-363-26	Sequence 26, Appli
17	36	54.5	120	4 US-09-100-089-26	Sequence 26, Appli
18	36	54.5	120	4 US-09-670-827-26	Sequence 26, Appli
19	36	54.5	269	4 US-09-082-649B-82	Sequence 82, Appli
20	36	54.5	271	1 US-07-977-630-5	Sequence 5, Appli
21	36	54.5	271	1 US-08-850-880-6	Sequence 6, Appli
22	36	54.5	271	2 US-08-944-916-5	Sequence 6, Appli
23	36	54.5	271	2 US-08-814-877-6	Sequence 6, Appli
24	36	54.5	271	4 US-08-760-615-8	Sequence 8, Appli
25	36	54.5	271	4 US-09-131-028A-5	Sequence 5, Appli
26	36	54.5	271	4 US-09-131-028A-7	Sequence 7, Appli
27	36	54.5	271	4 US-09-272-432A-6	Sequence 6, Appli

28	36	54.5	274	2 US-08-469-537A-55	Sequence 55, Appli
29	36	54.5	275	2 US-07-857-224B-71	Sequence 71, Appli
30	36	54.5	293	2 US-08-701-191A-26	Sequence 26, Appli
31	36	54.5	523	3 US-08-651-999A-2	Sequence 2, Appli
32	36	54.5	523	4 US-09-385-752-2	Sequence 228, App
33	36	54.5	837	4 US-09-564-805-228	Sequence 3, Appli
34	36	54.5	1255	3 US-08-947-823-3	Sequence 5, Appli
35	36	54.5	1257	3 US-08-947-823-5	Sequence 5, Appli
36	36	54.5	1614	4 US-09-052-469-2	Sequence 2, Appli
37	36	54.5	2213	1 US-08-727-034-3	Sequence 3, Appli
38	36	54.5	2214	1 US-08-727-034-7	Sequence 7, Appli
39	36	54.5	4302	3 US-08-658-136-5	Sequence 5, Appli
40	36	54.5	4302	4 US-09-052-469-8	Sequence 8, Appli
41	36	54.5	4303	2 US-08-460-751-2	Sequence 2, Appli
42	36	54.5	4339	4 US-09-052-469-6	Sequence 6, Appli
43	35.5	53.8	566	3 US-08-335-865J-9	Sequence 9, Appli
44	35.5	53.8	593	3 US-08-335-865J-21	Sequence 21, Appli
45	35	53.0	288	1 US-08-396-650-1	Sequence 1, Appli

## ALIGNMENTS

```

RESULT 1
US-09-643-597-176
Sequence 176, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-176
Query Match 100.0%; Score 66; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 FVDCPDESMAL 11
Db 41 FVDCPDESMAL 51
RESULT 2
US-09-643-597-348
Sequence 348, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.

```

APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 348  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-643-597-348

Query Match 100.0%; Score 66; DB 4; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0.0052;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDPSMAL 11  
DB 41 FVDCPDPSMAL 51

RESULT 3  
US-09-261-855-2  
Sequence 2, Application US/09261855A  
Patent No. 6255055  
GENERAL INFORMATION:  
APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261,855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 577  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-2

Query Match 89.4%; Score 59; DB 4; Length 577;  
Best Local Similarity 81.8%; Pred. No. 0.067;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FVDCPDPSMAL 11  
DB 41 FVDCPDPSMAL 51

RESULT 4  
US-09-109-205-1  
Sequence 1, Application US/09109205  
Patent No. 6057140  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Guegler, Karl J.  
APPLICANT: Gorgone, Gina  
APPLICANT: Corley, Neil C.  
APPLICANT: Baughn, Mariah R.  
APPLICANT: Yue, Henry  
TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,205  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0542 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGN0T14  
CLONE: 1511003  
US-09-109-205-1

Query Match 60.6%; Score 40; DB 3; Length 309;  
Best Local Similarity 85.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDPE 7  
DB 134 FVDCPDPE 140

RESULT 5  
US-08-261-822A-16  
Sequence 16, Application US/08261822A  
Patent No. 5650553  
GENERAL INFORMATION:  
APPLICANT: Ecker, Joseph R. et al.  
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene  
NUMBER OF SEQUENCES: 82  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 565053aris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,822A  
FILING DATE: 17-JUN-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Beigel, Lori Y.  
REGISTRATION NUMBER: 34,293  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 16:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-261-822A-16

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Query Match          57.6%; Score 38; DB 1; Length 398;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 VDCPDSESWAL 11
    1:1:11111:
Db 245 FLEYPPESWAV 255

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RESULT 6
PCT-US95-07744A-16
; Sequence 16, Application PC/TUS9507744A
; GENERAL INFORMATION:
; APPLICANT: Trustees of The University of Pennsylvania
; TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
; NUMBER OF INVENTION: and Pathogens
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07744A
; FILING DATE: 15-JUNE-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/261,822
; FILING DATE: June 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Beargell, Lori Y.
; REGISTRATION NUMBER: 34,293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US95-07744A-16

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Query Match          57.6%; Score 38; DB 5; Length 398;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 VDCPDSESWAL 11
    1:1:11111:
Db 245 FLEYPPESWAV 255

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RESULT 7

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US-09-564-805-2
; Sequence 2, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-805-2

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```

Query Match          57.6%; Score 38; DB 4; Length 826;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 2 VDCPDSESW 9
    1:1:11111:
Db 309 VECPDSEF 316

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RESULT 8
US-09-564-805-224
; Sequence 224, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 224
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-564-805-224

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Query Match          57.6%; Score 38; DB 4; Length 826;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 2 VDCPDSESW 9
    1:1:11111:
Db 309 VECPDSEF 316

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RESULT 9  
US-09-564-805-226

Thu Apr 17 07:55:20 2003

us-09-897-778-176\_copy\_41\_51.rai

Page 4

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/ Sequence 226, Application US/09564805
/ Patent No. 633403
/ GENERAL INFORMATION:
/ APPLICANT: Tavtigian, Sean V.
/ APPLICANT: Teng, David H.P.
/ APPLICANT: Simard, Jacques
/ APPLICANT: Rommens, Johanna M.
/ APPLICANT: Myriad Genetics, Inc.
/ TITLE OF INVENTION: Chromosome 17p-linked Prostate Cancer Susceptibility
/ FILE REFERENCE: 2318-258
/ CURRENT APPLICATION NUMBER: US/09/564,805
/ PRIOR FILING DATE: 2000-05-05
/ PRIOR APPLICATION NUMBER: US 60/107,468
/ PRIOR FILING DATE: 1997-11-06
/ PRIOR APPLICATION NUMBER: 09/434,382
/ NUMBER OF SEQ ID NOS: 240
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 826
/ LENGTH 826
/ TYPE: PRT
/ ORGANISM: Gorilla gorilla
US-09-564-805-226

Query Match 57.64; Score 38; DB 4; Length 826;
Best Local Similarity 75.04; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VDCPDESW 9
DB 309 VECPESEF 316

RESULT 10
US-09-149-476-707
/ Sequence 707, Application US/09149476
/ Patent No. 6420526
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 186 Human Secreted proteins
/ FILE REFERENCE: P2002p1
/ CURRENT APPLICATION NUMBER: US/09/149,476
/ PRIOR FILING DATE: 1998-09-08
/ PRIOR APPLICATION NUMBER: PCT/US98/04493
/ EARLIER FILING DATE: 1998-03-06
/ EARLIER APPLICATION NUMBER: 60/040,162
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,333
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/038,621
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,626
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,334
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,336
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,163
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/047,600
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,615
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,597
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,502
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,633
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,583
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,617

/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,618
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,503
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,592
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,581
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,584
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,500
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,587
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,492
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,598
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,613
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,582
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,596
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/043,568
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,314
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,569
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,311
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,671
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,674
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,669
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,312
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,313
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,672
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,315
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/056,886
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,877
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,889
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,893
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,630
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,878
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,662
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          56.1%; Score 37; DB 4; Length 430;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      4 CPDPSW 9
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Db      19 CPDPSW 24

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RESULT 11
US-09-564-805-222
; Sequence 222, Application US/09564805
; Patent No. 633403
; GENERAL INFORMATION:
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 822
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-805-222

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Query Match          56.1%; Score 37; DB 4; Length 822;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 VDCPDSESMAL 11
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Db      296 VDCPDSESMAL 305

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RESULT 12
US-09-342-648-9
; Sequence 9, Application US/09342648
; Patent No. 6248584
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Transcription Coactivators
; FILE REFERENCE: BB-1169-B

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Thu Apr 17 07:55:20 2003

us-09-897-778-176\_copy\_41\_51.ra1

Page: 6

;; CURRENT APPLICATION NUMBER: US/09/342,648  
;; CURRENT FILING DATE: 1999-06-29  
;; EARLIER APPLICATION NUMBER: 60/092,659  
;; EARLIER FILING DATE: July 13, 1998  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 9  
;; LENGTH: 885  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-342-648-9

Query Match 56.1%; Score 37; DB 4; Length 885;  
Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DCPDESWA 10  
DB 47 DTPDEPWA 54

RESULT 13  
US-08-777-405A-2  
;; Sequence 2, Application US/0877405A  
;; Patent No. 5858753  
;; GENERAL INFORMATION:  
;; APPLICANT: Chantry, David  
;; APPLICANT: Hoekstra, Merl F.  
;; APPLICANT: Holtzman, Douglas A  
;; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
;; NUMBER OF SEQUENCES: 17  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
;; STREET: 6300 Sears Tower/233 South Wacker Drive  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60606  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/777,405A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 5858753and, Greta E.  
;; REGISTRATION NUMBER: 35,302  
;; REFERENCE/DOCKET NUMBER: 27866/33441  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (312) 474-6300  
;; TELEFAX: (312) 474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1044 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-777-405A-2

Query Match 56.1%; Score 37; DB 2; Length 1044;  
Best Local Similarity 75.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VDCPDESW 9  
DB 5 VDCPMEFW 12

RESULT 14

US-08-977-871A-2  
;; Sequence 2, Application US/08977871A  
;; Patent No. 5882910  
;; GENERAL INFORMATION:  
;; APPLICANT: Chantry, David  
;; APPLICANT: Hoekstra, Merl F.  
;; APPLICANT: Holtzman, Douglas A  
;; TITLE OF INVENTION: No. 5882910el Lipid Kinase  
;; NUMBER OF SEQUENCES: 17  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
;; STREET: 6300 Sears Tower/233 South Wacker Drive  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60606  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/977,871A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/777,405  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 5882910and, Greta E.  
;; REGISTRATION NUMBER: 35,302  
;; REFERENCE/DOCKET NUMBER: 27866/33441  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (312) 474-6300  
;; TELEFAX: (312) 474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1044 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-977-871A-2

Query Match 56.1%; Score 37; DB 2; Length 1044;  
Best Local Similarity 75.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VDCPDESW 9  
DB 5 VDCPMEFW 12

RESULT 15  
US-09-225-951-2  
;; Sequence 2, Application US/09225951  
;; Patent No. 5985589  
;; GENERAL INFORMATION:  
;; APPLICANT: Chantry, David  
;; APPLICANT: Hoekstra, Merl F.  
;; APPLICANT: Holtzman, Douglas A  
;; TITLE OF INVENTION: No. 5985589el Lipid Kinase  
;; NUMBER OF SEQUENCES: 17  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
;; STREET: 6300 Sears Tower/233 South Wacker Drive  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60606  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; SOFTWARE: IBM PC compatible  
US-09-225-951-2

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,951  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5985589and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1044 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-225-951-2

Query Match 56.1%; Score 37; DB 2; Length 1044;  
Best Local Similarity .75.0%; Pred. NO. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Caps 0;  
QY 2 VDCPDSEW 9  
| | | | |  
Db 5 VDCPMEFW 12

Search completed: April 16, 2003, 16:22:59  
Job time : 1.61412 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:21:35 ; Search time 0.83087 Seconds  
(without alignments)  
1001.062 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66  
Sequence: 1 FVDCPDSESWAL 11

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEM\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEM\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEM\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEM\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	US-09-897-778-466	Sequence 466, App
2	66	100.0	18	US-09-897-778-465	Sequence 465, App
3	66	100.0	20	US-09-735-705-400	Sequence 400, App
4	66	100.0	20	US-09-850-716A-400	Sequence 400, App
5	66	100.0	20	US-09-897-778-400	Sequence 400, App
6	66	100.0	20	US-09-897-778-457	Sequence 457, App
7	66	100.0	579	US-09-735-705-116	Sequence 116, App
8	66	100.0	579	US-09-735-705-348	Sequence 348, App
9	66	100.0	579	US-09-850-716A-176	Sequence 176, App
10	66	100.0	579	US-09-850-716A-348	Sequence 348, App
11	66	100.0	579	US-09-897-778-176	Sequence 176, App
12	66	100.0	579	US-09-897-778-348	Sequence 348, App
13	66	100.0	579	US-09-897-778-446	Sequence 446, App
14	66	100.0	586	US-09-897-778-449	Sequence 449, App
15	66	100.0	586	US-09-850-716A-427	Sequence 427, App
16	66	100.0	586	US-09-897-778-427	Sequence 427, App
17	59	89.4	577	US-09-873-637-2	Sequence 2, Appli
18	58	87.9	20	US-09-735-705-399	Sequence 399, App
19	58	87.9	20	US-09-850-716A-399	Sequence 399, App

20	58	87.9	20	US-09-897-778-399	Sequence 399, App
21	47	71.2	620	US-09-764-864-1116	Sequence 1116, App
22	41	62.1	52	US-09-796-692-1087	Sequence 1087, App
23	41	62.1	52	US-09-796-692-1561	Sequence 1561, App
24	41	62.1	60	US-09-796-692-878	Sequence 878, App
25	41	62.1	68	US-09-796-692-687	Sequence 687, App
26	41	62.1	76	US-09-796-692-1076	Sequence 1076, App
27	41	62.1	82	US-09-796-692-1641	Sequence 1641, App
28	40	60.6	303	US-09-925-299-851	Sequence 851, App
29	40	60.6	303	US-09-925-299-851	Sequence 851, App
30	38	57.6	826	US-09-988-626-2	Sequence 2, Appli
31	38	57.6	826	US-09-988-626-224	Sequence 224, App
32	38	57.6	826	US-09-988-626-226	Sequence 226, App
33	38	57.6	826	US-09-988-687-2	Sequence 2, Appli
34	38	57.6	826	US-09-988-687-224	Sequence 224, App
35	38	57.6	826	US-09-988-687-226	Sequence 226, App
36	37	56.1	430	US-09-988-687-226	Sequence 707, App
37	37	56.1	560	US-09-809-391-707	Sequence 2, Appli
38	37	56.1	822	US-10-213-509-2	Sequence 222, App
39	37	56.1	822	US-09-988-626-222	Sequence 222, App
40	37	56.1	1044	US-10-028-072-234	Sequence 2, Appli
41	37	56.1	1160	US-10-028-072-234	Sequence 234, App
42	37	56.1	1160	US-10-121-049-234	Sequence 234, App
43	37	56.1	1160	US-10-123-904-234	Sequence 234, App
44	37	56.1	1160	US-10-140-470-234	Sequence 234, App
45	37	56.1	1160	US-10-175-746-234	Sequence 234, App

#### ALIGNMENTS

RESULT 1  
US-09-897-778-466  
Sequence 466, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Marnerakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.453C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 466  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-466  
Query Match  
Best Local Similarity 100.0%; Score 66; DB 10; Length 11;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVDCPDSESWAL 11  
DB 1 FVDCPDSESWAL 11  
RESULT 2  
US-09-897-778-465  
Sequence 465, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong

```

; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 2001-06-28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465
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Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 FVDCPDSESWAL 11
Db 5 FVDCPDSESWAL 15
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```

RESULT 3
; Sequence 400, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Pan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-400
```

```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```

RESULT 4
; Sequence 400, Application US/09850716A
; Patent No. US20020115139A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-400
```

```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```

RESULT 5
; Sequence 400, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 400
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-400
```

```
Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDSESWAL 11
Db 2 FVDCPDSESWAL 12
```

```

RESULT 6
; Sequence 457, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
```

```

: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897.778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 457
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-457

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 20;
Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
DB 2 FVDCPDESMAL 12

RESULT 7
US-09-735-705-176
: Sequence 176, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735.705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-176

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 579;
Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
DB 41 FVDCPDESMAL 51

RESULT 8
US-09-735-705-348
: Sequence 348, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
```

```

: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735.705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 348
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-735-705-348

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 579;
Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
DB 41 FVDCPDESMAL 51

RESULT 9
US-09-850-716A-176
: Sequence 176, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850.716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 176
: LENGTH: 579
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-176

Query Match
Best Local Similarity 100.0%; Score 66; DB 10; Length 579;
Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
DB 41 FVDCPDESMAL 51

RESULT 10
US-09-850-716A-348
: Sequence 348, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850.716A
: CURRENT FILING DATE: 2001-05-07
```

```
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-348
```

```
Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESML 11
Db      41 FVDCPDESML 51
```

```
RESULT 11
US-09-897-778-176
; Sequence 176, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-176
```

```
Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESML 11
Db      41 FVDCPDESML 51
```

```
RESULT 12
US-09-897-778-348
; Sequence 348, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348
```

```
Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESML 11
Db      41 FVDCPDESML 51
```

```
RESULT 13
US-09-897-778-446
; Sequence 446, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-446
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```
Query Match          100.0%; Score 66; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 FVDCPDESML 11
Db      41 FVDCPDESML 51
```

```
RESULT 14
US-09-897-778-449
; Sequence 449, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 449  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-897-778-449

Query Match 100.0%; Score 66; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 0.0042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||||  
DB 41 FVDCPDESMA 51

RESULT 15  
US-09-850-716A-427  
Sequence 427, Application US/09850716A  
Patent No. US20020115139A1  
GENERAL INFORMATION:  
APPLICANT: Kalos, Michael D.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716A  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 427  
LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-850-716A-427

Query Match 100.0%; Score 66; DB 10; Length 586;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||||  
DB 48 FVDCPDESMA 58

Search completed: April 16, 2003, 16:32:09  
Job time : 1.83087 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:19:20 : Search time 7.38752 Seconds  
(without alignments)  
960.006 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66  
Sequence: 1 FVDCPDSSMAL 11

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep:\*  
22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep:\*  
24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
27: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	1	PCT-US01-47576-466
2	66	100.0	11	22	US-09-897-778-466
3	66	100.0	11	24	US-10-007-700-466
4	66	100.0	11	25	US-10-117-982-466
5	66	100.0	18	1	PCT-US01-47576-465
6	66	100.0	18	22	US-09-897-778-465

7	66	100.0	18	24	US-10-007-700-465	Sequence 465, App
8	66	100.0	18	25	US-10-117-982-465	Sequence 465, App
9	66	100.0	20	1	PCT-US01-47576-400	Sequence 400, App
10	66	100.0	20	1	PCT-US01-47576-457	Sequence 457, App
11	66	100.0	20	21	US-09-735-705-400	Sequence 400, App
12	66	100.0	20	22	US-09-850-716-400	Sequence 400, App
13	66	100.0	20	22	US-09-850-716A-400	Sequence 400, App
14	66	100.0	20	22	US-09-897-778-400	Sequence 400, App
15	66	100.0	20	22	US-09-897-778-457	Sequence 457, App
16	66	100.0	20	24	US-10-007-700-400	Sequence 400, App
17	66	100.0	20	24	US-10-007-700-457	Sequence 457, App
18	66	100.0	20	25	US-10-117-982-400	Sequence 400, App
19	66	100.0	20	25	US-10-117-982-457	Sequence 457, App
20	66	100.0	43	25	US-10-117-982-482	Sequence 482, App
21	66	100.0	579	1	PCT-US01-47576-176	Sequence 176, App
22	66	100.0	579	1	PCT-US01-47576-348	Sequence 348, App
23	66	100.0	579	1	PCT-US01-47576-446	Sequence 446, App
24	66	100.0	579	1	PCT-US01-47576-449	Sequence 449, App
25	66	100.0	579	18	US-09-466-396A-176	Sequence 176, App
26	66	100.0	579	18	US-09-476-496A-176	Sequence 176, App
27	66	100.0	579	18	US-09-480-884A-176	Sequence 176, App
28	66	100.0	579	19	US-09-510-376A-176	Sequence 176, App
29	66	100.0	579	19	US-09-542-615A-176	Sequence 176, App
30	66	100.0	579	19	US-09-542-615A-348	Sequence 348, App
31	66	100.0	579	20	US-09-606-421A-176	Sequence 176, App
32	66	100.0	579	20	US-09-606-421A-348	Sequence 348, App
33	66	100.0	579	20	US-09-606-421B-176	Sequence 176, App
34	66	100.0	579	20	US-09-606-421B-348	Sequence 348, App
35	66	100.0	579	20	US-09-630-940A-176	Sequence 176, App
36	66	100.0	579	20	US-09-630-940A-348	Sequence 348, App
37	66	100.0	579	20	US-09-630-940B-176	Sequence 176, App
38	66	100.0	579	20	US-09-630-940B-348	Sequence 348, App
39	66	100.0	579	20	US-09-662-786-176	Sequence 176, App
40	66	100.0	579	20	US-09-662-786-348	Sequence 348, App
41	66	100.0	579	20	US-09-685-696-176	Sequence 176, App
42	66	100.0	579	20	US-09-685-696-348	Sequence 348, App
43	66	100.0	579	21	US-09-735-705-176	Sequence 176, App
44	66	100.0	579	21	US-09-735-705-348	Sequence 348, App
45	66	100.0	579	21	US-09-791-537-49019	Sequence 49019, A

## ALIGNMENTS

RESULT 1

Sequence 466, Application PC/TUS0147576

GENERAL INFORMATION:

APPLICANT: Corixa Corporation

APPLICANT: Wang, Tonglong

APPLICANT: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Li, Samuel X.

APPLICANT: Kalos, Michael D.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

APPLICANT: Retter, Marc W.

APPLICANT: Durham, Margarita

APPLICANT: Fanger, Gary R.

APPLICANT: Vedick, Thomas S.

APPLICANT: Carter, Darick

APPLICANT: Matanabe, Yoshinori

APPLICANT: Peckman, David W.

APPLICANT: Cal, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.45503PC

CURRENT APPLICATION NUMBER: PCT/US01/47576

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FASTSEQ for Windows Version 4.0

```

; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-466
Query Match          100.0%; Score 66; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 2
US-09-897-778-466
; Sequence 466, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Beckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-466
Query Match          100.0%; Score 66; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 3
US-10-007-700-466
; Sequence 466, Application US/10007700
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Beckham, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-466
Query Match          100.0%; Score 66; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 4
US-10-117-982-466
; Sequence 466, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-466
Query Match          100.0%; Score 66; DB 25; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 5
PCT-US01-47576-465
; Sequence 465, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
```

```

; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-466
Query Match          100.0%; Score 66; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 4
US-10-117-982-466
; Sequence 466, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-466
Query Match          100.0%; Score 66; DB 25; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMAL 11
Db 1 FVDCPDESMAL 11

RESULT 5
PCT-US01-47576-465
; Sequence 465, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
```

```

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47576-465
```

```
Query Match          100.0%; Score 66; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15
```

## RESULT 6

```
US-09-897-778-465
; Sequence 465, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455016
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-465
```

```
Query Match          100.0%; Score 66; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15
```

## RESULT 7

```
US-10-007-700-465
; Sequence 465, Application US/10007700
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Reller, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cal, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455017
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-465
```

```
Query Match          100.0%; Score 66; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15
```

## RESULT 8

```
US-10-117-982-465
; Sequence 465, Application US/10117982
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455018
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-465
```

```
Query Match          100.0%; Score 66; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FVDCPDDESMAL 11
DB 5 FVDCPDDESMAL 15
```

## RESULT 9

```
PCT-US01-47576-400
; Sequence 400, Application PC/TUS0147576
```

```

GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Wang, Tonglong
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margailta
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Watanabe, Yoshihito
APPLICANT: Peckman, David W.
APPLICANT: Cal, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.45503PC
CURRENT APPLICATION NUMBER: PCT/US01/47576
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 400
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-47576-400

Query Match
Best Local Similarity 100.0%; Score 66; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1  FVNCPEPSMAL 11
        |||||
Db      2  FVDCPEPSMAL 12

RESULT 10
PCT-US01-47576-457
Sequence 457, Application PC/TUS0147576
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Wang, Tonglong
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margailta
APPLICANT: Fanger, Gary R.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Watanabe, Yoshihito
APPLICANT: Peckman, David W.
APPLICANT: Cal, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.45503PC
CURRENT APPLICATION NUMBER: PCT/US01/47576
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 457
LENGTH: 20
TYPE: PRT

```

```

1 ORGANISM: Homo sapiens
2 PCT-US01-47576-457
3
4 Query Match 100.0%; Score 66; DB 1; Length 20;
5 Best Local Similarity 100.0%; Pred. No. 0.0019;
6 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
7
8 QY 1 FVDCPDESMA1 11
9 |||||||||
10 DB 2 FVDCPDESMA1 12
11
12
13 RESULT 11
14 US-09-735-705-400
15 : Sequence 400, Application US/09735705
16 : GENERAL INFORMATION:
17 : APPLICANT: Wang, Tongtong
18 : APPLICANT: Fan, Liqun
19 : APPLICANT: Kalos, Michael D.
20 : APPLICANT: Bangur, Chaltanya S.
21 : APPLICANT: Hosken, Nancy
22 : APPLICANT: Fanger, Gary R.
23 : APPLICANT: Li, Samuel X.
24 : APPLICANT: Wang, Aijun
25 : APPLICANT: Skeiky, Yasir A.W.
26 : APPLICANT: Henderson, Robert A.
27 : APPLICANT: McNeill, Patricia D.
28 : APPLICANT: Fanger, Neil
29 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
30 : FILE REFERENCE: 210121.455C14
31 : CURRENT APPLICATION NUMBER: US/09/735,705
32 : CURRENT FILING DATE: 2000-12-12
33 : NUMBER OF SEQ ID NOS: 419
34 : SOFTWARE: FastSeq for Windows Version 3.0
35 : SEQ ID NO. 400
36 : LENGTH: 20
37 : TYPE: PRT
38 : ORGANISM: Homo sapiens
39
40 US-09-735-705-400
41
42 Query Match 100.0%; Score 66; DB 21; Length 20;
43 Best Local Similarity 100.0%; Pred. No. 0.0019;
44 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
45
46 QY 1 FVDCPDESMA1 11
47 |||||||||
48 DB 2 FVDCPDESMA1 12
49
50
51 RESULT 12
52 US-09-850-716-400
53 : Sequence 400, Application US/09850716
54 : GENERAL INFORMATION:
55 : APPLICANT: Wang, Tongtong
56 : APPLICANT: Fan, Liqun
57 : APPLICANT: Kalos, Michael D.
58 : APPLICANT: Bangur, Chaltanya S.
59 : APPLICANT: Hosken, Nancy
60 : APPLICANT: Fanger, Gary R.
61 : APPLICANT: Li, Samuel X.
62 : APPLICANT: Wang, Aijun
63 : APPLICANT: Skeiky, Yasir A.W.
64 : APPLICANT: Henderson, Robert A.
65 : APPLICANT: McNeill, Patricia D.
66 : APPLICANT: Fanger, Neil
67 : APPLICANT: Retter, Marc W.
68 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
69 : FILE REFERENCE: 210121.455C15
70 : CURRENT APPLICATION NUMBER: US/09/850,716
71 : CURRENT FILING DATE: 2001-05-07
72 : NUMBER OF SEQ ID NOS: 440

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SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 400  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716-400

Query Match 100.0%; Score 66; DB 22; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||  
DB 2 FVDCPDESMA 12

RESULT 13  
US-09-850-716A-400  
; Sequence 400, Application US/09850716A  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Reiter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 400  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-400

Query Match 100.0%; Score 66; DB 22; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||  
DB 2 FVDCPDESMA 12

RESULT 14  
US-09-897-778-400  
; Sequence 400, Application US/09897778  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Marnetakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 400  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-400

Query Match 100.0%; Score 66; DB 22; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FVDCPDESMA 11  
|||  
DB 2 FVDCPDESMA 12

RESULT 15  
US-09-897-778-457  
; Sequence 457, Application US/09897778  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Marnetakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-457

Query Match 100.0%; Score 66; DB 22; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESMA 11  
|||  
DB 2 FVDCPDESMA 12

Search completed: April 16, 2003, 16:29:54  
Job time : 7.38752 secs





GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: April 16, 2003, 16:19:55 ; Search time 1.35468 Seconds  
(without alignments)  
1266.170 Million cell updates/sec

Title: US-09-897-778-176\_COPY\_41\_51

Perfect score: 66

Sequence: 1 FVDCPDESMAL 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 705215 seqs, 155932251 residues

Total number of hits satisfying chosen parameters: 705215

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA.New:\*  
1: /cgn2\_6/ptodata/1/paa/PCIT\_NEW.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW.COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	US-10-313-986-466	Sequence 466, App
2	66	100.0	18	US-10-313-986-465	Sequence 465, App
3	66	100.0	20	US-10-313-986-400	Sequence 400, App
4	66	100.0	20	US-10-313-986-457	Sequence 457, App
5	66	100.0	20	US-10-313-986-508	Sequence 508, App
6	66	100.0	43	US-10-313-986-482	Sequence 482, App
7	66	100.0	134	US-09-724-676-92917	Sequence 92917, A
8	66	100.0	134	US-09-724-676A-92917	Sequence 92917, A
9	66	100.0	492	US-09-724-676-92916	Sequence 92916, A
10	66	100.0	492	US-09-724-676A-92916	Sequence 92916, A
11	66	100.0	558	US-09-724-676-92918	Sequence 92918, A
12	66	100.0	558	US-09-724-676A-92918	Sequence 92918, A
13	66	100.0	579	US-10-313-986-176	Sequence 176, App
14	66	100.0	579	US-10-313-986-348	Sequence 348, App
15	66	100.0	579	US-10-313-986-446	Sequence 446, App
16	66	100.0	579	US-10-313-986-449	Sequence 449, App
17	66	100.0	579	US-10-313-986-480	Sequence 480, App
18	66	100.0	579	US-10-313-986-484	Sequence 484, App
19	66	100.0	579	US-10-348-119-255	Sequence 255, App
20	66	100.0	589	US-10-313-986-427	Sequence 427, App
21	66	100.0	589	US-10-313-986-486	Sequence 486, App
22	59	89.4	572	US-09-724-676-48617	Sequence 48617, A
23	59	89.4	572	US-09-724-676A-48617	Sequence 48617, A
24	59	89.4	572	US-09-724-676A-48617	Sequence 48617, A
25	59	89.4	572	US-09-724-676A-48618	Sequence 48618, A
26	59	89.4	577	US-10-313-986-500	Sequence 500, App

27	59	89.4	598	5	US-09-724-676-48616	Sequence 48616, A
28	59	89.4	598	5	US-09-724-676A-48621	Sequence 48621, A
29	59	89.4	598	5	US-09-724-676A-48616	Sequence 48616, A
30	59	89.4	598	5	US-09-724-676A-48621	Sequence 48621, A
31	59	89.4	602	5	US-09-724-676-48619	Sequence 48619, A
32	59	89.4	602	5	US-09-724-676-48620	Sequence 48620, A
33	59	89.4	602	5	US-09-724-676A-48619	Sequence 48619, A
34	59	89.4	602	5	US-09-724-676A-48620	Sequence 48620, A
35	58	87.9	20	6	US-10-313-986-399	Sequence 399, App
36	58	87.9	20	6	US-10-313-986-470	Sequence 470, App
37	58	87.9	20	6	US-10-313-986-507	Sequence 507, App
38	47	71.2	97	5	US-09-513-999C-7342	Sequence 7342, App
39	47	71.2	255	7	US-60-452-680-15601	Sequence 15601, A
40	47	71.2	555	1	PCT-US02-31357-40	Sequence 40, Appl
41	47	71.2	555	6	US-10-262-445-40	Sequence 40, Appl
42	47	71.2	556	7	US-60-453-135-11528	Sequence 11528, A
43	47	71.2	556	7	US-60-453-050-11528	Sequence 11528, A
44	47	71.2	587	6	US-10-313-986-501	Sequence 501, App
45	47	71.2	599	7	US-60-453-135-11527	Sequence 11527, A

## ALIGNMENTS

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RESULT 1
US-10-313-986-466
Sequence 466, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313.986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 466
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-313-986-466

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 FVDCPDESMAL 11
1 FVDCPDESMAL 11
US-10-313-986-465
Sequence 465, Application US/10313986
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313.986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 465
LENGTH: 18

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Thu Apr 17 07:55:21 2003

us-09-897-778-176\_copy\_41\_51.rapn

Page 2

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-465

Query Match 100.0%; Score 66; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 5 FVDCPDESVAL 15

RESULT 3  
US-10-313-986-400

Sequence 400, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19  
CURRENT APPLICATION NUMBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04  
NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 400

LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-400

Query Match 100.0%; Score 66; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 2 FVDCPDESVAL 12

RESULT 4  
US-10-313-986-457

Sequence 457, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19  
CURRENT APPLICATION NUMBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04  
NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 457

LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-457

Query Match 100.0%; Score 66; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 2 FVDCPDESVAL 12

RESULT 5  
US-10-313-986-508

Sequence 508, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19  
CURRENT APPLICATION NUMBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04  
NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 508

LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-508

Query Match 100.0%; Score 66; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 2 FVDCPDESVAL 12

RESULT 6  
US-10-313-986-482

Sequence 482, Application US/10313986  
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.  
APPLICANT: McNabb, Andria  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19  
CURRENT APPLICATION NUMBER: US/10/313,986

CURRENT FILING DATE: 2002-12-04  
NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 482

LENGTH: 43  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-986-482

Query Match 100.0%; Score 66; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDESVAL 11  
Db 9 FVDCPDESVAL 19

RESULT 7  
US-09-724-676-92917

Sequence 92917, Application US/09724676  
GENERAL INFORMATION:

APPLICANT: Compugen LTD.  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92917

Query Match 100.0%; Score 66; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 8  
US-09-724-676A-92917  
Sequence 92917, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92917  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92917

Query Match 100.0%; Score 66; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 9  
US-09-724-676-92916  
Sequence 92916, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92916

Query Match 100.0%; Score 66; DB 5; Length 492;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 10  
US-09-724-676A-92916  
Sequence 92916, Application US/09724676A  
GENERAL INFORMATION:

APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92916  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92916

Query Match 100.0%; Score 66; DB 5; Length 492;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 11  
US-09-724-676-92918  
Sequence 92918, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-92918

Query Match 100.0%; Score 66; DB 5; Length 558;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

RESULT 12  
US-09-724-676A-92918  
Sequence 92918, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 92918  
LENGTH: 558  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-92918

Query Match 100.0%; Score 66; DB 5; Length 558;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVDCPDDESML 11  
Db 41 FVDCPDDESML 51

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RESULT 13
US-10-313-986-176
; Sequence 176, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-176

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 579;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 14
US-10-313-986-348
; Sequence 348, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-348

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 579;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

RESULT 15
US-10-313-986-446
; Sequence 446, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-446

Query Match
Best Local Similarity 100.0%; Score 66; DB 6; Length 579;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVDCPDSESMAL 11
Db 41 FVDCPDSESMAL 51

Search completed: April 16, 2003, 16:31:16
Job time : 2.35466 secs

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